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Result
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Perfect score:
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                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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9 US-09-908-602-76
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APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30

US 60/234,687

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US-09-860-670-161

US-09-860-670-161

; Sequence 161, Application US/09860670

; Patent No. US20020165137A1

; GENERAL INFORMATION:
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US-09-910-943-287/c
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NUMBER OF SEQ ID NOS: 742
SOFTWARE: PatentIn version 3.1
SEQ ID NO 287
LENGTH: 709
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Patent No. US20020081610A1
GENERAL INFORMATION:
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SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 7775
LENGTH: 527
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TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REFERENCE: 7529/1G148US1
CURRENT APPLICATION NUMBER: US/09/910,943
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Altman, Curtis
APPLICANT: Ruben et al
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NAME/KEY: misc_feature
LOCATION: (1)..(709)
OTHER INFORMATION: n may be a
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ORGANISM: Xenopus laevis
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HELA, SIGNAL = 5.2
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FETAL LIVER, SIGNAL = 4.5
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Publication No.
Query Match
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CURRENT FILING DATE: 2001-03-01
CURRENT PPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mannion, Jane
TITLE OF INVENTION: CONSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 289
                                                                                                                                                                                                                 NUMBER OF SEQ ID N
SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/200,545 PRIOR FILING DATE: 2000-04-27
                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(309)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 26555
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 2000-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/
FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/200,779
                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/
FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/223,416
                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-05-
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/200,303
                                                                                                                                                                                                                                                                                        [LING DATE: 2000-08-04
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                                                                                                                                                                                                                 for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                             NUMBER: 60/218,950
2000-07-14
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100.0%;
4.5%;
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Pred. No.
Score 17;
Pred. No.
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US-09-796-692-3533
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            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3533, Application US/09796692 Publication No. US20020198362A1
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
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PRIOR FILING DATE: 2000-04-27
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PRIOR FILING DATE: 2000-03-17
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PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIOR APPLICATION NUMBER:
                                                                                  OTHER INFORMATION: n=A,T,C or
                                                                                                                                   LOCATION: (289)
OTHER INFORMATION: n-A,T,C or
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (11)
OTHER INFORMATION: n-A,T,C
                                                                                                  NAME/KEY: unsure
LOCATION: (296)
                                                                                                                                                                                                                                                               NAME/KEY: unsure LOCATION: (272)
                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                       NAME/KEY: unsure
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LOCATION: (277)
                                                                                                                                                                                                                                           OTHER INFORMATION: n-A,T,C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/200,999
FILING DATE: 2000-05-01
APPLICATION NUMBER: 60/202,084
FILING DATE: 2000-05-04
APPLICATION NUMBER: 60/206,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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          Score 17; Pred. No.
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          DB 9;
12;
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                           Length 309;
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; OTHER INFORMATION: unsure at all n locations; OTHER INFORMATION: Clone ID: LIB3028-009-01-B1-B5
US-09-878-574-3537
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US-10-040-739-843/c
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Best Local S
Matches 17
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SEQ ID NO 3537
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
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PRIOR FILING DATE: 1999-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 TCTGGAGCTGAAGGATG 119
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                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                 CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
                                                                                                                                                                                COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    La Rosa, Ti
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacobs, Kenneth
                                                                                                                                                                                                                                                                                       Spaulding, Vikki
VENTION: SECRETED,
EQUENCES: 1519
                                                                                                                                                                                                                                                                                                                                             Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                          Merberg,
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Lavallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                Racie, Lisa
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                                                                                                                                                                                                                                                                                                           EXPRESSED SEQUENCE TAGS
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12;
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Gaps

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GENERAL INFORMATION:
APPLICANT: Leach, Ma
APPLICANT: Mehraban
APPLICANT: Conley,
APPLICANT: Law, Deb
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                                                                                                                                                                                                                                                                                                                              US-09-938-842A-1704
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                                                                                       Patent No.
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1704
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                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                          Query Match
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PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS,
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                      LENGTH: 837
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 876-58
INFORMATION FOR SEQ ID NO: 843:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           610 GAGATGCCAATCCATGG 594
                                                                                                                                                                                         276 TGAAAAGAGACCTTTGG 292
                                                                                                                                                                                                                           229 TGAAAAGAGACCTTTGG 245
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                                                                                                                                                                                                                                                                            Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,520
EILING DATE: 03-JUN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                     1051, Application US/09867550 o. US20020082206A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity
17; Conserv
 Leach, Martin D.
Mehraban, Fuad,
Conley, Pamela
Law, Debbie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 627 base pairs
                                                                                                                                                                                                                                                           Conservative
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100.0%; Pr
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                                                                                                                                                                                                                                                                            4.5%; Score 17;
100.0%; Pred. No.
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Pred. No.
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12;
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; COTHER INFORMATION: wherein any n is one of a US-09-867-550-1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-864-761-31616/c
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Best Local Similarity
Matches 17; Conserv
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TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cell
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/00669 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04 PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR FILING DATE: 2000-09-27
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                                                                                                                  PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
                                                                                                PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1005
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                                                                                                                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                      APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00663
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                                         2001-01-30
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Pred. No.
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RESULT 12
US-09-739-254-13/c
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; Sequence 3427, Application US/09938842A
; Patent No. US20020160378A1
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                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
Sequence 13, Application US/09739254 Patent No. US20010021700A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31616
LENGTH: 1041
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                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3427
LENGTH: 1359
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Best Local
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN HELIOD, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.93

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.9

OTHER INFORMATION: SWISSPROT HIT: 934910, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: 934910, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: AA805896.1, EVALUE 0.00e+00
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TYPE: DNA
ORGANISM: Homo saplens
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                                                                                                                         531 GAGTCTCTCACAAGCTT 515
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les 17; Conserv
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les 17; Conservative
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Pred. No.
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US-09-864-761-15087/c

Sequence 15087, Application US/09864761 Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G. APPLICANT: Rank, David K. APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng RESULT 14

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TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/739,254
CURRENT ETLING DATE: 2000-12-19
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: PCT/US99/19330
EARLIER APPLICATION NUMBER: E07/0599/19330
EARLIER FILING DATE: 1999-08-24
EARLIER FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 60/097,917
EARLIER APPLICATION NUMBER: 60/098,634
EARLIER APPLICATION NUMBER: 60/098,634
EARLIER APPLICATION NUMBER: 60/098,634
EARLIER APPLICATION NUMBER: 60/098,634
                                                                                                                                                         ; TYPE: DNA; ORGANISM: Homo sapiens US-09-904-615-13
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US-09-904-615-13/c
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SEQ ID NO 13
LENGTH: 1666
TYPE: DNA
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Matches 17; Conserva
                                                                                                                                                                                                                                       SEQ ID NO 13
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                                                                                                                Query Match
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CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al. TITLE OF INVENTION: 49 Human Secreted Proteins FILE REFERENCE: PZ032P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 170
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                                                                                                                                                                                                                ENGTH:
                    271 GATGCCAATCCATGGAA 287
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740 GATGCCAATCCATGGAA 724
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nes 17; Conserv
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100.0%; Pred. No.
1tive 0; Mismatal
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OTHER INFORMATION: EXPRESSED IN HBL100,
OTHER INFORMATION: EXPRESSED IN PLACEMYZ
OTHER INFORMATION: EXPRESSED IN FETAL L1
OTHER INFORMATION: EXPRESSED IN LUNG, S1,
OTHER INFORMATION: EXPRESSED IN BONE MAI
US-09-864-761-15087
                                                                                                                                                     RESULT 15
US-09-808-602-76/c
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PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR ELLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
                                               APPLICANT: Vernet,
                                                                                                 Sequence 76, Application US/09808602 Patent No. US20020155115A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 15087
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Best Local (
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APPLICANT:
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TURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IOR APPLICATION NUMBER: PCT/USO1/00662
IOR APPLICATION NUMBER: PCT/USO1/00661
IOR APPLICATION NUMBER: PCT/USO1/00661
IOR APPLICATION NUMBER: PCT/USO1/00670
IOR APPLICATION NUMBER: PCT/USO1/00670
IOR APPLICATION NUMBER: US 60/234,687
IOR APPLICATION NUMBER: US 60/234,687
IOR APPLICATION NUMBER: US 99/608,408
IOR APPLICATION NUMBER: US 99/608,408
IOR APPLICATION NUMBER: US 99/774,203
IOR APPLICATION NUMBER: US 99/774,203
IOR APPLICATION NUMBER: US 99/774,203
IOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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                                                 Vernet, Corine A
Fernandes, Elma
Shimkets, Richard
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IN FETAL LIVER, SIGNAL = 0.93
IN LUNG, SIGNAL = 2.6
IN BONE MARROW, SIGNAL = 4.9
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-808-602-76
                                                                                                                                                                          SEQ ID NO 76
                                                         Matches
                                                                     Query Match
Best Local
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                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                       APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Sar
FILE REFERENCE: 15966-697 CIP
                                                                                                                                                                                         SOFTWARE:
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l Similarity
17; Conserv
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                                                           Conservative
                                                                     4.5%; Score 17;
100.0%; Pred. No.
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13;
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Search completed: January 31, 2003, 05:19:41 Job time : 345 secs

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Title:
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seg length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           January 31, 2003, 01:19:33;
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                                 /cgn2_6/ptodata/1/1na/5A_COMB.seq: *
/cgn2_6/ptodata/1/1na/5B_COMB.seq: *
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US-08-480-910-6
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US-09-250-569-1
US-09-260-569-1
US-09-261-474-9
US-09-261-474-9
US-09-315-609-4
US-09-315-609-4
US-09-315-372-4
US-09-344-752-4
US-09-345-497-4
US-09-345-497-4
US-09-356-919-4
US-09-563-919-4
US-09-563-919-4
US-09-563-919-4
US-09-563-919-3
US-08-735-609-1
US-08-735-609-1
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US-08-735-609-1
US-09-315-372-1
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US-09-345-497-1
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Compugen Ltd
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Sequence 1, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 11, Appli
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Sequence 1, A
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	л <b>-</b> л -	Sequence 3, Appl	Sequence 31, App		Sequence 23, Appl		Sequence 23, A			2 2	, N	24	10,		) <u>-</u>	1 7 8

ALIGNMENTS

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RESULT 1
US-09-134-001C-1264
Sequence 1264, Application US/09134001C
Patent No. 6380370
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCO
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1264
LENGTH: 1080
                                                                                                                                                                              Sequence 6, Application US/08480910

Patent No. 5693530

GENERAL INFORMATION:
APPLICANT: Karel A. Schat, Kazuhiko Ohashi, and Priscilla APPLICANT: H. O'Connell
TITLE OF INVENTION: A Marek's Disease Virus Nucleotide TITLE OF INVENTION: Sequence and Methods of Use
Patent No. 5693530

NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 17; Conserv
                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ,
STREET: 1800 One M6T Plaza
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 GTAGCTATAGCAGAAGT 325
                                                               STREET: 1800 OF CITY: Buffalo STATE: New York
                      COUNTRY: United ZIP: 14203-2391
                                                                 New York
                                           United States
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100.0%; Pred. No. 14
Live 0; Mismatches
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                                                                                                                                                Woods & Goodyear
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US-09-257-580-1
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                                                         US-09-257-580-4
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         Sequence 4, Application US/09257580 Patent No. 6307036 GENERAL INFORMATION:
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                                                                                                                                                                          Matches
                                                                                                                                                                                                    Query Match
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TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/257,580 CURRENT FILING DATE: 1999-02-25 PRIOR APPLICATION NUMBER: 9804178.3 PRIOR FILING DATE: 1998-02-28
                                                                                                                                                                                                                                                                                        LENGTH: 1146
TYPE: DNA
ORGANISM: Canis
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Tumour Suppressor Gene FILE REFERENCE: Canine p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: U.S. Serial No. 5693530 08/180,051 FILING DATE: 11 January 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect for Windows 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                  1007
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                                                                                                                                            105 TGGAGCTGAAGGATGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS/
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COMPUTER: II
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                                                                                                                                                                                        Local Similarity
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                                                                                                                  TGGAGCTGAAGGATGC 1022
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Yorkshire Cancer Research
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No.
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US-09-257-580-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81...
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: Canine p53
CURRENT APPLICATION NUMBER: US/09/257,580
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5693530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1146
TYPE: RNA
                                                                                                                                                                                                               TELEFAX: (716) 849-0349 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1007 UGGAGCUGAAGGAUGC 1022
                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS/ Microsoft Windows SOFTWARE: Wordperfect for Windows 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U.S. Serial No. 5693530 08/180,051 FILING DATE: 11 January 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                             ORIGINAL SOURCE:
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ent No. 5693530
NUMBER OF SEQUENCES:
                                                                                             MOLECULE TYPE: cD
                                                         IMMEDIATE SOURCE:
LIBRARY: CDNA
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STREET: 1
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/480,910 FILING DATE: 07 June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Buffalo
                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RY: United States
14203-2391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08480910
                                                                                                                                                              nucleic acid
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                                                clone L1
: Marek's Disease Virus MDCC-CU41
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1800 One M&T Plaza
                                                                                                                                                                              1285 nucleotides
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                                                                                                                                                                                                                              (716)
                                                                                                                                 linear
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                                                                                                                                                                                                                             849-0349
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81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Marek's Disease Virus Nucleotide Sequence and Methods of Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5 inch, 1.44Mb storage
                                                                                                                                                                                                                                                                                18617.0005
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; LOCATION: L1 open reading frame, 725-1045; IDENTIFICATION METHOD: by experiment; OTHER INFORMATION:
US-08-480-910-1
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Query Match
                                                                                                                                    CLONE: CLONE L1
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                           TELEFAX: (716) 849-0349
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Control Of Marek's Disease By The
                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 08/180,051
FILING DATE: January 11, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                761 AGGAACATATGGAAAA 776
                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: CDNA
                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
ZIP: 142
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Local Similarity 100.0%;
es 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hodgson, Russ, Andrews, Woods & ADDRESSEE: Goodyear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Buffalo
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                                            LOCATION: L1 open reading IDENTIFICATION METHOD: by OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                            CELL TYPE:
                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                    ropoLogy: linear
                                                                                                                                                                                                                                                                                                  ENGTH:
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14203-2391
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                                                                                                                                                                                                                                                                                 nucleic
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                                                                                                        narek's Disease Virus
MDCC-CU41
E: virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karel A. Schat, Kazuhiko Ohashi, and Priscilla H. O'Connell
                                                                                                                                                                                                                                                                                                1285 nucleotides
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                                                                                                                                                                                                                                       CDNA
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   4.2%;
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Pred. No.
    Score 16;
                                                            frame, 725-1045 experiment
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    DB 5;
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; LOCATION: (1302)
US-09-500-569-17
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US-09-500-569-17/c
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                                                                                                                                                                                                  Sequence 9, Application US/09461474 Patent No. 6278042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1999-February-10 NUMBER of SEQ ID NOS: 28 SOFTWARE: Microsoft Office 97 EQ ID NO 17
          NUMBER OF SEQ ID NOS
SOFTWARE: Microsoft
SEQ ID NO 9
                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 60/119,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1314
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cahoon, Rebecca E.
                                                                                  APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
                                                     EARLIER APPLICATION NUMBER: 60/112,562 EARLIER FILING DATE: 1998-12-16
                                                                                                                                                                        APPLICANT: Allen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure LOCATION: (472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                         1247 CCCAAGCCGGAGTCTC 1232
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(1262)
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(1180)
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                              Office 97
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Pred. No.
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US-09-461-474-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-09-221-017B-811/c
                           US-09-221-0178-811
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Best Local Similarity
Matches 16; Conserv
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Query Match
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                                                                                                                                                                                                TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4413 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASCOTO DATE:
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
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APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
                                                                        FEATURE:
                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                             HYPOTHETICAL:
                                                                                                                                          MOLECULE TYPE:
                                                                                                                 NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 755 PAGE
CITY: Palo Alto
                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: doub
                                          NAME/KEY: misc_feature LOCATION: 1...4413
                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,430 REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                               NAME: MONTOY, Gladys
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                     ORGANISM:
                                                                                                                                                            TOPOLOGY:
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                                                                                                                 UNKNOWN
                                                                                     PORYPHYROMONAS GINGIVALIS
                                                                                                                                                         circular
                                                                                                                                                                                                                                                                                                                                                            10-DEC-1998
                                                                                                                                        DNA (genomic)
                                                                                                                                                                       double
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Pred. No.
                                                                                                                                                                                                                                                                                                      27340-20021.00
Score 16;
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43
DB
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Length 4413;
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US-09-318-448-11
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US-08-735-609-4/c
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Sequence 11, APP1-
Sequence 11, APP1-
Sequence 11, APP1-
No. 6210950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%; | Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Johnson, William G.
APPLICANT: Stentroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 46
INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 18596
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10134 GATGGTGATGGAGATG 10149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                           TELEPHONE: (415) 705-8410
                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,
                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 GATGGTGATGGAGATG 274
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                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Medlen & Carroll, LLP
STREEF: 220 Montgomery Street, St
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                      FILING DATE:
                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chamberlain, Jeffrey
Amalfitano, Andrea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kumar-Singh, Rajendra
                                                                                                                                                                                                                      IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                     us/08/735,609
                                                                                    40,027
                                                                                                                                                                                                                                                                                                       Of America
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                                                                 UM-02484
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; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      Suite 2200
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US-08-735-609-4/c
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                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserv
27052 CAACATGCTTTGACTG 27037
                                                                                                                                                                                                                TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27052 CAACATGCTTTGACTG 27037
                                  212 CAACATGCTTTGACTG 227.
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LENGTH: 34303 base pai
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                                                                                  Local
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                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ingolla, Diane E.
                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kumar-Singh, Rajendra
Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chamberlain, Jeffrey
                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                 NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08735609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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ilarity 100.0%; Pred. No.
Conservative 0; Mismatri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 Montgomery Street, Suite 2200
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                                                                                4.2%;
                                                                   0,
                                                                                Score 16;
Pred. No.
                                                                   Mismatches
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37;
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                                                                                              Length 34303;
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RESULT 14
US-09-244-752-4/c
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US-09-315-372-4/c
                                                                                                                                                                                    Sequence 4, Applic Patent No. 6063622
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Matches
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                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pa1
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                                                                                                                                                                                                                                                                                          27052 CAACATGCTTTGACTG 27037
                                 CORRESPONDENCE ADDRESS:
                                                             APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: UM TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/315,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          212 CAACATGCTTTGACTG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Medlen & Callul, Suite STREET: 220 Montgomery Street, Suite CITY: San Francisco STATE: California Crates Of America
 STREET:
                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States Of America ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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16; Conserv
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nucleic acid
                                                                                                                                                                                                       Application US/09244752
2: Medlen & Carroll, LLP
220 Montgomery Street, Suite 2200
                                                                                               Amalfitano, Andrea
Hauser, Michael A.
Kumar-Singh, Rajendra
                                                                                                                                                    Chamberlain, Jeffrey
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               other nucleic acid
/desc = "DNA"
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100.0%; Pred. No.
tive 0; Mismatci
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ZIP: 9410%
COMPUTER READABLE FORM:
TYPE: Floppy disk

STATE: California COUNTRY: United States Of America

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US-09-245-497-4/c
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NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPEAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
INCOMPANION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09245497 Patent No. 6083750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.2%; Score 16; Best Local Similarity 100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27052 CAACATGCTTTGACTG 27037
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hauser, Michael APPLICANT: Kumar-Singh, Rajendra APPLICANT: Kumar-Singh, Rajendra APPLICANT: Hartigan-O'Connor, Dennis J. TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: Medlen & Carroll, LLP ADDRESSEE: Medlen & Carroll, LLP
               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
APPLICATION NUMBER:
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TOPOLOGY: linear
MOLECULE TYPE: othe
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/244,752
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 CAACATGCTTTGACTG 227
                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                         FILING DATE:
                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                              94104
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                 08/735,609
<B) FILING DATE:
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; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-09-245-497-4
Search completed: January 31, 2003, 03:51:24
Job time: 133 secs
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                                                                                                                         Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 397-83 INFORMATION FOR SEQ ID NO:
                                                            27052 CAACATGCTTTGACTG 27037
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UM-02484 TELECOMMUNICATION INFORMATION:
                                                                                          212 CAACATGCTTTGACTG 227
                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ingolia, Diane E. REGISTRATION NUMBER: 4(
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                                                                                                                        4.2%; Score 16; llarity 100.0%; Pred. No. Conservative 0; Mismatch
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Maximum DB seq length: 2000000000
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                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                              Score
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49
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30
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378
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gb_est2:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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AA743908
AI459918
BG197212
AQ035618
AQ035738
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BM987874 UI-H-CO0-
AA743908 ob05b10.s
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ALIGNMENTS

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BQ604599 BI184120 BE769032 AV610564 BI186343

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BG210731 BQ597872 BG223756 AV605455 AV605117 BF713089 AW464207 A2364217 BQ600629

RESULT 1 BM987874/c

	FEATURES Source	
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Seq primer: M13 FORWARD		
Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Jose Mercuende CDNA Library preparation: Dr. M. Bento Soares, University of Iowa		
Unpublished (1997) Contact: Robert Strausberg, Ph.D.	COMMENT	
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	TITLE	
<pre>i (Dases 1 to 451) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicqap.</pre>	AUTHORS	
Eukaryota; Metazoà Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Homo sapiens	ORGANISM	
-)	SOURCE	
BM987874.1 GI:19707263	VERSION KEYWORDS	
IMAGE:5860149 3', mRNA sequence. BM987874	ACCESSION	
-asz-a-11-0-UI.sl NCI_CGAP_Sub9 Hom	DEFINITION	
BM987874 451 bp mRNA linear	LOCUS	

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RESULT 2
AA743908/c
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AUTHORS
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                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Insert Length: 508 Std Error: 0
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                                                                                                                                           Seq primer: -40ml3 fwd.
High quality sequence st
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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1. (bases 1 to 386)
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                                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                            Tumor Gene Index
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                                                                                                                     quality sequence stop: 234.
Location/Qualifiers
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Cholonic mucosa with Crohns disease, Cholonic mucosa with
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
carcinoma, Bladder carcinoma, Brain oligodenroga;
NCI_CGAP_Sub9 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are CGTC, AACG, GGGCC,
GGAAG, TAGC, TAACC, ATGC, ATGAC. For additional
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1322779"
/clone_lib="NCI_CGAP_Kid3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_SEQ-ATGG"
93 c
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TAG_LIB=UI-H-CO0
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100.0%; Pr
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp mRNA linear EST 19-FEB-1998 sapiens cDNA clone IMAGE:1322779 3',
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hes 0;
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FEATURES

Query Match

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COMMENT

TITLE

SOURCE VERSION

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AUTHORS
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VERSION
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AI459918/c
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Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Mart
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylle,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                     Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI459918 439 bp mRNA linear EST ar81h09.xl Barstead colon HPLRB7 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.linl.gov) for Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
     115
                                                                                                                                                                                                                                                                                                                                              quality sequence stop:
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     a
                            /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI Sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                    /clone_lib="Barstead colon HPLRB7"
                                                                                                                                                                                                                                                        /clone="IMAGE:2151713"
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                    dev_stage="adult, age 25"
                                                                                                                                                                                                                      /sex="male"
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b; Pred. No. 2.9
0; Mismatches
81 g
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                                                                                  GSS
                                                                                                                                               AQ035618
CIT-HSP-2319N3.TF
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1 (bases 1 to 806)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Kilka, A., Hess, J., Cothren, K., Lo, K., Offenbacher (J., Danzig, J. and Ducar, M. Creation of genome wide protein expression libraries using random Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                AQ035618.1
                                                                                                                 AQ035618
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: scain@athersys.com
High quality sequence stop: 417
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Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Scott J. Cain
Atherays, Inc.
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RST16451 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG197212
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a 187 c 155 g 205 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HTI080"
/cell_line="HTI080"
/coll_specification of Genome-wide Protein Expression
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..5.7e-14;
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Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                             Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, F. Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other_GSSS: CIT-HSP-2321C21.TR
                                                                                                           Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CIT-HSP-2321C21.TF CIT-HSP Homo
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Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mark Adams
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Other_GSSs: CIT-HSP-2319N3.TR
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/db_xref="taxon:9606"
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C., Shizuya,H.,
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Kilka, A., Hess, J., Cothren, K., Lo, K., Offenbacher
                                                                                                                                                                                                                                                                                                                                                                                                                      Athersys, Inc.
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RST30277 Athersys RAGE Library |
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30; Conserv
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                                                                                                                                            136
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                          quality sequence stop:
Location/Qualifiers
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216 431 9900
216 361 9596
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                       scain@athersys.com
                                                                                                                                            8
                                                                                                                                       /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_llb="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2321C21"
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                                                                              5.6%;
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                                                                           Score 21; DB 12; Length 357; Pred. No. 1.7;
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Pred. No.
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                                                               red. No. 1.
Mismatches
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1.3e-05;
hes 0;
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                                    DEFINITION
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ACCESSION
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BQ597872/c
LOCUS
                                                                                                                                                                                                                                                      Query Match 5.6%; Sometive 0; Matches 21; Conservative 0;
                                                                                                                                                                                CDNA 5', mRNA sequence.
BG223756
BG223756.1 GI:12709277
EST.
                                                                    1M00018F10a Bovine Mixed
                                                                                              BG223756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Dr. Chris Tuggle, Iowa State University cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA sequence: 1-22, >AT_rich#Low_complexity

Seq_primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Towa State University
201 Kildee Hall, Ames, IA 50011-3150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular Genetics Laboratory, Department
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MI-P-A2-afh-a-04-1-UM.s', mRNA sequence
BQ597872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYA-Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 5152942401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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TAG_SEQ=TCGCGTT

82 C
                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-Ac library is derived from anterior pituitary at estrus contact of the library from withis clone was derived, please visit our web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9823"
/clone="MI-P-A2-afh-a-04-1-UM"
/clone_11b="MI-P-A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="crossbreed"
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Skeletal Muscle cDNA Library
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                                                          Bos taurus
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Best Local (
     JOURNAL
                                                    TITLE
                                                                                     AUTHORS
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AV605455.1
                                                                    and Sugimoto,Y.
                                                                                 Takasuga, A.,
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                 Bos taurus
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Bos taurus
                  DOVING ESTS
                                  poly(A) tail-removed
                                                                                                                   Bovi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA's from bovine mixed skeletal muscle Unpublished (2001) Contact: Dr. Stephen S. Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 526)

Moore, S. S., Hansen, C., Li,C., Fu,A., Meng,Y., Li,G., Mur Dixon,W. and Christopherson,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Dept of AFNS, University of Alberta
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780 492 4265
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                           lishment of a high throughput EST sequencing system
A) tall-removed cDNA libraries and determination of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="muscle"
/dev_stage="Young adult"
/lab_host="XL1-BlueWRF-strain"
/note="Organ: Skeletal muscle; Vector: Uni-2ZAPXR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                semimembrances"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Bovine Mixed Skeletal Muscle cDNA Library"
/sex="two males and one female mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="masseter, longissmusclorsi, biceps femoris,
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                   GI:9735828
                                                                              Hirotsune, S., Itoh, R., Jitohzono, A.,
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99 c 119 g :
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(22),
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                                                                              Suzuki, H., Aso, H.
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                                                                                                                              Bovoidea;
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COMMENT
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AV605117/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3', mRNA sequence.
AV605117
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AV605117
                                                                                                                                                                                                                                                                                                                                             Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 boving ESTS
                                                                                                                                                                                                                                  Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                    Single pass sequencing.
                                                                                                                                                                                                Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                            Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV605117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single pass sequencing.
This clone was obtained from a
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Odakura, Nishigo, Nishi-shirakawa, Fukushima Tel: 81-248-25-5641
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Shirakawa Institute of Animal Genetics
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Contact: Yoshikazu Sugimoto
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                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 545)
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                                                                                                                                                  clone was obtained from a polyA-deleted Location/Qualifiers
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                                             /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="ElKI026H04"
/clone_lib="Bos taurus k
/tissue_type="kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus kidney fetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
a 136 c 110 g 153 t 3 others
                  'lab_host="DH10B"
                                   /dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Bos taurus
/tissue_type="kidney"
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="fetus"
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Pred.
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Sall; Site_2: Not1; Poly A
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BF713089/c
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     Query Match 5.6%; Score 21; DB 12; Length 547; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cktuggleeiastate.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized hypothalamus at estrus day 12 library cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Preparation: Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: Clones will be
                                                                                                                                                                                                                                                                                                                                                                                                                                    Missouri-Columbia, 65211 Clone distribution: Gioues available through Research Genetics (www.resgen.com) Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF713089 547 bp mRNA linear ES' MI-P-H3-adm-h-03-1-UM.sl MI-P-H3 Sus scrofa cDNA clone MI-P-H3-adm-h-03-1-UM 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Towa State University
2001 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pig.
Sus scrofa
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BF713089.1 GI:12012570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Tuggle CK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Euthoria; Cetartiodactyla; Suina; Suidae; Sus.
(bases 1 to 547)
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                                                                                                                                                         /lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoR; The MI-P-H3 library is derived from hypothalamus at estrus day 12. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.lastate.edu/.
TAG_LIB-MI-P-H3
                                                                                                       TAG_TISSUE-hypothalamus at estrus day 12
TAG_SEQ-GGTTAA"
107 c 102 g 181 t
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                                                                                                                                                                                                                                                                                                     | strain="crossbreed"
|/db_xref="taxon:9823"
|/clone="MI-P-H3-ddn-h-03-1-UM"
|/clone_11b="MI-P-H3"
                                                                                                                                                                                                                                                                                                                                                                              /organism-"Sus scrofa"
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Pred. No.
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1.8;
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AUTHORS
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AW464207
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350 GAAGGAAGGTACCATTGGAGA 370
                                                                                         Local Similarity 100.
nes 21; Conservative
GAAGGAAGGTACCATTGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: h-levin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center Trimm1 9: Cross_match from Washington University Genome Center PHRAP Suite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 569.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: AGCGGATAACAATTTCACACAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross_match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 217 333 5998
Fax: 217 244 5617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP230015A10F9 Soares normalized bovine placenta Bos taurus cDNA clone BP230015A10F9 5', mRNA sequence.

AW464207
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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                                                                                                                                                                                                                160
                                                                                                                                                                                               /note-"Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NoLI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. *

a 112 c 144 g 150 t 3 others
                                                                                                                                                                                                                                                                                                                                                    /sex="female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP230015A10F9"
                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares normalized bovine placenta"
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252
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Pred. No.
                                                                                            Mismatches
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                                                                                                             DB 10;
1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dr., Urbana,
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589 bp

DNA

linear

GSS 02-OCT-2000

DEFINITION

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                  524 CTTTGACTGTTGAAAAGAGAC 544
                                                                                                                                                             219 CTTTGACTGTTGAAAAGAGAC 239
       BQ600629
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                                                                                                                                                                                                               Similarity 100
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0110 row: P column: 18
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: P column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Roye, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 589)
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                                                                                                                                                                                                                                                                                                              was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWH02 (91|4732114/gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for amplcillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0110P18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                             100.0%;
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Pred. No. 1.8;
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Search completed: January 31, 2003, 05:14:00 Job time: 2258 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
434 GAAGGAAGGTACCATTGGAGA 414
                                            350 GAAGGAAGGTACCATTGGAGA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cktuggle@lastate.edu
Tissue Procurement: Dr. Chris Tuggle, Iowa State University
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Cenetics (www.resgen.com)
Genetics (www.resgen.com)
The following repetitive elements were found in this cDNA
sequence: 1-22, >AT_rich#Low_complexity
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 611)
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                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Normalization and subtraction: two approaches to facilitate gene
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                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                      /clone_lib="MI-P-E7"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pSPORTI; Site_1: Not I; Site_2: EcoRI; The MI-P-E7 library is derived from the following tissue(s): preelongation day 12 conceptus. For a detailed description of the library from which this clone was derived, please visit our web site as the content of the library from which this clone was derived, please visit our web site as the content of the library from which this clone was derived, please
                                                                                                                                                                                                                    TAG_TISSUE=preelongation_d_12_conceptus TAG_SEO=GTGAGA"
                                                                                                                                                                                                                                                                 visit our web site at http://pigest.genome.lastate.edu/.
TAG_LIB=MI-P-E7
                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-E7-agz-d-10-1-UM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                              5.6%;
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                                                                                      0;
                                                                                                              Score 21; DB 14;
Pred. No. 1.8;
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                                                                                        Mismatches
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                                                                                                                                   Length 611;
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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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Copyright (c) 1993 - 2003 Compugen Ltd
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981, DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982, DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983, DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984, DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985, DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986, DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987, DAT:*
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AAS37237
AAS37218
AAS37242
ABA20368
ABA20369
ABA29309
ABA29309
AAK09951
AAK35845
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Novel human diagno
Human foetal liver
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Human brain expres
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		Arabidopsis thalia	Drosophila melanog	Staphylococcus epi	Human genome-deriv	Probe #9558 used t	E #1/903	m enod	1000	500	TIGTI A7	UGT1A7		Human UGT1A7 relate	Human polynucleoti	Arabidopsis thalia	Human neuroblastom	M. capsulatus gene	EST clone DD211.	Human prostate exp	Human haematologic			'Human immune/haema	Human immune/haema				Porcine muscular s	Porcine muscular s	Human immune/haema	Human immune/haema	Human nervous syst	_	•	#10349	Ť	

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## ALIGNMENTS

AAS37164 standard; cDNA; 378

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17-DEC-2001 AAS37164;

(first entry)

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YX Williams LT, Escobedo J, Innis MA, G Reinhard C, Randazzo F, Kennedy GC, Drmanac R, Crkvenjakov R, Dickson M, Leshkowitz D, Kita D, Garcia V, Jone WPI; 2001-530177/58 (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC. 09-MAR-2000; 2000US-0188609 09-MAR-2001; 2001WO-US07787 13-SEP-2001. WO200166753-A2 Homo sapiens Human; cancer; breast; Novel human diagnostic and therapeutic gene #222 lung; colon; prostate; cytostatic; diagnostic; ss Jones WL, Garcia PD, Sudduth-Klinger J;
POT D, Kassam A, Lamson G;
M, Drmanac S, Labat I;
Nnes WL, Stache-Crain B;

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AAS37237
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Best Local S
Matches 378
                      09-MAR-2000; 2000US-0188609
                                            09-MAR-2001;
(CHIR ) CHIRON CORF
                                                                                          WO200166753-A2
                                                                                                               Homo sapiens
                                                                                                                                                    Novel human diagnostic and therapeutic gene #295
                                                                                                                                     Human; cancer;
                                                                                                                                                                                17-DEC-2001
                                                                                                                                                                                                                          AAS37237 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to new polynucleotides and polypeptides, useful fo diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a differentially expressed genes correlated with a differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS3938 represent movel human diagnostic and therapeutic coding
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ilarity 100.0%;
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Pred. No. 1.6e-187;
Mismatches 0;
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                                                                                                                               prostate; cytostatic;
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Matches 238; Conserv
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                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic and therapeutic gene #276.
                                            (HYSE-)
                                                                    (CHIR )
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Reinhard C, Randazzo F, Kennedy GC, Pc
Drmanac R, Crkvenjakov R, Dickson M, F
Leshkowitz D, Kita D, Garcia V, Jones
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                                                               CHIRON CORP
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lung and colon cancer -
                                                                                                                                                                                                                                                                                                                                   lung; colon;
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Pred. No. 2.6e-114;
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es WL, Stache-Crain
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ssam A, Lamson (
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Williams LT,

Escobedo

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Innis MA,

Garcia

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Sudduth-Klinger

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RESULT
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Best Local Similarity
                             Williams LT,
Reinhard C,
Drmanac R, C
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                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic and therapeutic gene #300.
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Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotides and polypeptides, useful thent of breast, lung and colon cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAAACACCCAAGCCGGAGTCTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAAACACCCAAGCCGGAGTCTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGAT 111
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                                                                                                                   CHIRON CORP
HYSEQ INC.
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    ', Escobedo J, Innis MA,
Randazzo F, Kennedy GC,
Crkvenjakov R, Dickson M,
D, Kita D, Garcia V, Jor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Crkvenjakov i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 92
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Garcia PD, Sudduth-Kl
Pot D, Kassam A, Lan
, Drmanac S, Labat I;
nes WL, Stache-Crain B
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: S, Labat I;
                                                                Sudduth-Klinger
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04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000;

; 2000US-0179065. ; 2000US-0180628. ; 2000US-0184664. ; 2000US-0186350. ; 2000US-0189874.

31-JAN-2000; 17-JAN-2001; 16-AUG-2001

2001WO-US01334

Homo sapiens WO200159063-A2

neurological disease;

infection;

nephrotropic; gene therapy;

vaccine;

gb

immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulno antiparkinsonian; antisickling; antianaemic; antiarchritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticorvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; antiparasitic; cardiant; immune disorder; cardiovascular disorder;

ng; antianaemic; antiarthritic; cancer; cerebroprotective; antiinflammatory;

dermatological;

virucide;

antibacterial; vulnerary;

Human; nootropic; neuroprotective; cytostatic; immunosuppressive; antiinflammatory; anti-HIV;

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ABA20368
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                                                                                                                                                                                                                 Human nervous system related polynucleotide SEQ
                                                                                                                                                                                                                                         23-JAN-2002
                                                                                                                                                                                                                                                             ABA20368;
                                                                                                                                                                                                                                                                             ABA20368 standard; DNA; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with differentially expressed genes correlated with differentially expressed gene product in a test sample derived from a teall suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS3938 represent novel human diagnostic and therapeutic coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 318 BP; 90 A; 63 C; 76 G;
                                                                                                                                                                                                                                                                                                                                 247
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                                                                                                                                                                                                                                                                                                                                                                                                            127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the invention.
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Pred. No.
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18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000;

2000US-0198123.
2000US-0209467.
2000US-0216486.
2000US-0216687.
2000US-0216880.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0218290.
2000US-0218290.
2000US-0224519.
2000US-0224519.
2000US-0225214.
2000US-0225266.
2000US-0225276.
2000US-022527757.
2000US-0225758.
2000US-0225759.
2000US-02257757.
2000US-02257759.
2000US-02257759.

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RAPER PRESENTED TO THE REPORT OF THE REPORT 
The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are
                                                                                                                                                                                                                                                                                                                               17-NOV-2000

01-DEC-2000

01-DEC-2000

05-DEC-2000

05-DEC-2000

05-DEC-2000

06-DEC-2000

06-DEC-2000

08-DEC-2000

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08-DEC-2000

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08-DEC-2000

08-DEC-2000
                                                                                              Disclosure;
                                                                                                                                Nucleic acids encoding useful for preventing, cancers and metastases
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17-NOV-2000
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08-NOV-2000
08-NOV-2000
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                                                                                                                                                                                                                                                       CA,
                                                                                                                                                                                                                                                                                            HUMAN
                                                                                              SEQ
                                                                                                                                                                                                                                                   Barash SC,
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2000US-0241809
2000US-0241809
2000US-0246474
2000US-0246475
2000US-0246477
2000US-0246477
2000US-0246478
2000US-0246523
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2000US-0249216
2000US-0249216
2000US-0249216
2000US-0251160
2000US-02511866
2000US-0251866
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2000US-0251999
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2000US-0241785
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                                                                             12699; 1701pp + Sequence Listing; English.
                                                                                                                                     3224 human
diagnosing
                                                                                                                                                                                                                                                   Ruben
                                                                                                                                                                                                                                                   MS
                                                                                                                                       nervous system antigen polypeptides, and/or treating nervous system
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14 - AUG - 2000)
16 - SEP - 2000)
17 - SEP - 2000)
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2000US-0226681
2000US-0226681
2000US-0227109
2000US-0229343
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2000US-0231244
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2000US-0231244
2000US-0231244
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2000US-0231244
2000US-0231244
2000US-0231268
2000US-0232080
2000US-0232080
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2000US-0234274
2000US-0234284
2000US-0236367
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2000US-0237038

SSXS

printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence

527 BP; 175 A;

99

C

110 G;

143 T; 0 other;

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RESULT 6
ABA61650
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                               04-FEB-2000; 2000US-0180312.
25-MAY-2000; 2000US-0207456.
30_UM-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rhemmatoid arthritis and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                     Claim 1; SEQ ID NO
                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; foetal liver;
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                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human foetal liver single exon nucleic acid probe #9955.
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                                                                                                                                                                                                                           SG,
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 The sequence data
                                                                                                                                                             genome-derived single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
                                                                                                                                               ome-derived single exon nucleic acid probes useful gene expression in human fetal liver -
                                                                                                                                                                                                                         Hanzel DK,
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                                                                                                               9955; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression; single exon nucleic acid probe;
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for this patent did not form
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Pred. No.
                                                                                                                                                                                                                         Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 T; 0 other;
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9;
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                                                                                                                English.
part of the
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                               measuring human gene expression in a sample derived from human heart. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system. Gradiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                               specification,
                                           Note:
                                                                                                                                                        Claim 1; SEQ
                                                                                                                                                                                        Single
                                                                                                                                                                                                                                 Penn
                                                                                                                                 The present invention relates to single exon nucleic acid
                                                                                                                                                                              hearts
                                                                                                                                                                                                             WPI; 2001-488899/53
                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                          04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                         congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene expression; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #7775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA29309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA29309 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 TGTTCTTTGGAATAAAAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                  ftp.wipo.int/pub/published_pct_sequences.
                           The sequence data for this patent did not fication, but was obtained in electronic for
                                                                                                                                                                                                                                 , os
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                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                       nucleic
                                                                                                                                                                                                                                                                                  ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for gene expression analysis in human heart cell sample.
                                                                                                                                                      ID No 7775; 530pp; English.
                                                                                                                                                                                                                                                                         2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                        2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                                                     acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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                                                                                                                                                                                                                              Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527
                                                                                                                                                                                                                                                                                                                                                                                                                                                 heart; microarray; vas
hypertension; cardiac
                                                                                                                                                                                   probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495
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Pred. No.
                                                                                                                                                                                                                               Rank
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                                                                                                                                                                                                                               DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         vascular system; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                            format
                                                                                                                                                                                                                                                                                                                                                                                                                                                 arrhythmia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o,
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                           directly
                                                         vascular system
hmias and
                                                                                                                                  probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                           om WIPO
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Query Match Matches

Local

l Similarity 19; Conserv

Conservative

5.0%; 50 100.0%; Pr

Score 19; DB; Pred. No. 9; 0; Mismatches

9; 8g

0

Indels

0

Gaps

0;

22;

Length 527;

Sequence 527

BP; 175

A; 99 C; 110 G; 143 T;

0 other;

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RESULT 9
AAK35845
ID AAK3
XX
AC AAK3
XX
DT 06-N
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AAK09951
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                                                                                                                   Matches
                                                                                                                            Query Match
Best Local 9
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
  06-NOV-2001
                    AAK35845;
                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                             Single
brains
                                     AAK35845
                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                     Sequence 527
                                                                                                                                                                                                                                       Example 4; SEQ ID NO: 9942; 650pp +
                                                                                        162 TGTTCTTTGGAATAAAAAC
                                                                                                                                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed e microarray; Alzheimer's
                                                                                   477
                                                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK09951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK09951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162
                                                                                                                                                                                                                                                                                                                                                           -SEP-2000;
                                                                                TGTTCTTTGGAATAAAAAC 495
                                                                                                                                                                                                                                                                                                        SG,
                                                                                                                                                                                                                                                                                      2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTCTTTGGAATAAAAC
                                                                                                                  l Similarity
19; Conserv
                                                                                                                                                                                                                                                                 exon nucleic acid probes for analyzing
                                     standard;
                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                        2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed single
(first entry)
                                                                                                                                                      BP; 175
                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.
                                     DNA;
                                                                                                              5.0%; Pr
100.0%; Pr
                                                                                                                                                    A; 99 C;
                                                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon;
                                     527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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                                                                                                                          Score 19;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                    110 G; 143 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                      Rank
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression analysis; probe; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probe
                                                                                                                                                                                                                                      Sequence Listing; English.
                                                                                                                                                                                                                                                                                                      DR;
                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                  22;
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                                                                                                                 0
                                                                                                                                                   other;
                                                                                                                                                                                                                                                                  gene expression
                                                                                                                                Length 527;
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RESULT 10
AAI17155
ID AAI17157
XX AAI17
XX 12-OC
XX 12-OC
XX Probe
XX Probe
XX Cervi
XX Cervi
XX Homo
XX Homo
XX W0200
XX W0200
XX W0200
XX W0300
XX W0300
XX W0300
XX W04-FF
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                     Matches
                                           09-AUG-
04-FEB-2000; 2000US-0180312
                                                                                                                                   Probe #7088 for gene expression analysis in human cervical cell sample.
                     30-JAN-2001; 2001WO-US00670.
                                                                 WO200157278-A2
                                                                                      Homo sapiens
                                                                                                           cervical
                                                                                                                                                             12-OCT-2001
                                                                                                                                                                                   AAI17155;
                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic ac probes which are derived from genomic sequences expressed in the bone marrow. They can be used to measure gene expression in bone samples, which may enable the improved diagnosis and treatment of such as lymphoma, leukaemia and myeloma. The present sequence is the probes of the invention.
                                                                                                                                                                                                      AAI17155 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                            477
                                                                                                                                                                                                                                                                   162 TGTTCTTTGGAATAAAAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                         TGTTCTTTGGAATAAAAAC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone marrow expressed single exon
                                                                                                                      human;
                                                                                                                                                                                                                                                                                                    l Similarity
19; Conserv
                                                                                                          uman; microarray; gene expression; cervical epithelial cell;
cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                              527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                              B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000GB-0024263
                                                                                                                                                                                                                                                                                                                                        175 A; 99 C; 110 G; 143 T; 0 other;
                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed exon; gene expression ar; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                            5.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    10402; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                      527
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                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon nucleic acid probes useful n human bone marrow -
                                                                                                                                                                                                                                                                                                              Score 19;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DR;
                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe
                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                                                     Length 527;
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                                                                                                                                                                                                                                                                                                                                                                     of cancers
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he human
                                                                                                                                                                                                                                                                                               Gaps
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RESULT 11
AAI41562
ID AAI41
XX AAI41
XX AAI41
XX Probe
XX Probe
XX Probe
XX Probe
XX Genet
XX
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                                                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to human single exon nucleic acid probes (SEMP). The present sequence is one such probe. The SEMPs are derived from human HeLa cells. The SEMPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #10248 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                   WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI41562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI41562 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 TGTTCTTTGGAATAAAAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             local
                        SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTCTTTGGAATAAAAAC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; SEQ ID No 7088; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
19; Conserv
                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULAR DYNAMICS INC
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                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                           2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0632368.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.0%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-02346359.
; 2000US-0234263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 175 A; 99 C; 110 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
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Pred. No
                   Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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RESULT 12
ABS10078
ID ABS10
XX ABS10
XX ABS10
XX ABS10
XX ABS10
XX ID-AU
XX
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                               Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples -       
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary hastiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary cillary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon probe from lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                   2002-114183/15.
                                                                                                                                                                                                                                                        SG
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 527
                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                   2000US-180312P.
2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
2000US-236359P.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.0%; Solitarity 100.0%; If Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 A; 99 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB; Pred. No. 9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 G; 143 T; 0 other;
                                                                                                                                                                                                                                                      Rank
                                                                                                                                                                                                                                                   DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID No 10069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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The invention relates to nucleic acid probes for m

o a spatial measuring

spatially-addressable : asuring gene expression

set of on in a s

single

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derived exon Claim 1;

SEQ ID No 10069; 634pp; English.

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RESULT 13
ABA17906
ID ABA17
XX ABA17
XX ABA17
XX ABA17
XX Human
XX Human
XX Human
XX Human
XX inmur
KW inmur
KW antig
KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC mRNA, and (b) measuring the label detectably bound to each probe of CC (a) algorithmically predicting at least one exon from genomic sequences CC (a) algorithmically predicting at least one exon from genomic sequences CC of the eukaryote; and (b) detecting specific hybridisation of detectably CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, CC having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, CC comprising (a) identifying exons from genomic sequence by the method CC above and (b) measuring the expression of each of the exons in several CC tissues and/or cell types using hybridisation to a single exon cc microarrays having a probe with the exon, where a common pattern of CC expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one CC of 12011 sequences, mentioned in the specification, or encoded by the CC probes/open reading frames (ORF). The probes are used for gene cexpression analysis, and for identifying exons in a gene, particularly CC using human lung derived mRNA and for the study of lung diseases (CCOPD), interstital lung disease (ILD), familial idiopathic pulmonary disease. CC (COPD), interstital lung disease (ILD), familial idiopathic pulmonary CC haemosiderosis, pulmonary histocytosis, lumphangioleiomyomtosis, pulmonary disease, Permansky-Pudlak syndrome, sarcoidosis, pulmonary CC haemosiderosis, pulmonary histocytosis, lumphangioleiomyomtosis, caucher's disease. The prosesor sequence is a single exon CC pulmonary disease. The present sequence is a single exon CC pulmonary disease. The present sequence is a single exon CC pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 19
                                                                                                                                                                        Human; nootropic; neuroprotective; cytostatic; dermatological; virusimunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulne antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiuleer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring the array with a collection of detectably labeled nucleic acids derived from human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the printed specification, but format directly from WIPO at
                                                            WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA17906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA17906 standard; DNA; 9929 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                            Homo sapiens
                                                                                                                                                           neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wlpo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention.

The sequence data for this patent did

The sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                   nervous system
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                related polynucleotide SEQ
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                                                                                                                                                      infection; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No
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BB
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                                                                                                                                                    gene therapy;
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                                                                                                                                                      vaccine;
                                                                                                                                                                                                                                                                        vulnerary;
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     14-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
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29-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

05-SEP-2000

06-SEP-2000

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11-SEP-2000

11-SEP-2000

14-SEP-2000

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14-SEP-2000

14-SEP-2000
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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19-MAY-2000;
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17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                          2000US - 0230437

2000US - 0230438

2000US - 0231242

2000US - 0231243

2000US - 0231244

2000US - 0231413

2000US - 0231414

2000US - 0231414

2000US - 0231414

2000US - 0232080

2000US - 0232080

2000US - 0232081

2000US - 0232997
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2000US-0227182.
2000US-0227109.
2000US-0228924.
2000US-0229287.
2000US-0229287.
2000US-0229343.
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                                                         Rosen CA,
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                                                   Ruben SM;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are considered from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune (b) immune disorders e.g. haddison's disease, allergies, autoimmune colisses, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) woud healing; (e) neurological diseases e.g. cerebral anoxia and cepliepsy; and (f) infectious diseases such as myocardial ischaemias; and lepsy; and (f) infectious diseases such as viral, bacterial, fungal cand parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 10237; 1701pp + Sequence Listing; English.
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Query Match
Best Local Similarity
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                    AAK58913 standard; cDNA; 249 BP
                                                                                            128 TTAAGCCCCTGTTCTTTTC 146
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                                                                                                                                        5.0%; Score 19;
100.0%; Pred. No.
                                                                                                                               0;
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8.7;
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Sequence 9929 BP; 2748 A; 1678 C; 1979 G; 3524 T; 0 other;

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Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3973.
                                                           06-NOV-2001 (first entry)
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.

W0200157182-A2 Homo sapiens.

RESULT 14
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ID AAK5891
XX AAK589
XX O6-NOV
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KW Cytost
XX Homo s.
XX WO2001
XX Homo s.
XX Homo s.
XX Homo s.
XX PN WO2001
XX 17-JAN
PR 04-FEB
PR 04-FEB
PR 17-MAR
PR 11-MAR
PR 11-JUL
PR 11-JU 07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000; 11-JUL-2000; 31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 17-JAN-2001; 2001WO-US01354 09-AUG-2001. 2000US-0179065 2000US-0180628 2000US-0184664 2000US-0186350 2000US-019974 2000US-0198123 2000US-0198123 2000US-0203467 2000US-0203467 2000US-0214886 2000US-0215135 2000US-0216847 2000US-0216880 2000US-0217487 2000US-0217487 2000US-0217487 2000US-0217487

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08-NOV-2000
17-NOV-2000
17-NOV
AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent,
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08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                Nucleic acids encoding useful for preventing, metastasis -
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P-PSDB; AAM86132.
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26-JUL-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 12-AUG-2000 12-AUG-2000 13-AUG-2000 13-AUG-2000 13-AUG-2000 14-AUG-2000 13-AUG-2000 14-SEP-2000 15-SEP-2000 16-SEP-2000 16-SEP-2000 16-SEP-2000 16-SEP-2000 17-SEP-2000 18-SEP-2000 18-SEP-2000 18-SEP-2000 18-SEP-2000 18-SEP-2000 18-SEP-2000 19-SEP-2000 11-SEP-2000 11-SE

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XX
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XX
Cytostatic; gene therapy; vacc
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PN W0200157182-A2.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC concerns the patients and polynucleotides may be used to protein and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC cancers and cancer metastases of haematopoletic-related diseases, especially CC cancers and cancer metastases of haematopoletic antigen genomic concerns sequences used in the exemplification of the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                     Query Match
Best Local
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17-NOV-2000;
17-NOV-2000;
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01-DEC-2000;
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05-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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17-NOV-2000;
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                                                                                                          Sequence 333 BP; 84 A; 91 C; 64 G; 94 T; 0 other;
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                                                   4.8%; Silarity 100.0%; Conservative 0;
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2000US-0251479.
2000US-0251856.
2000US-0251869.
2000US-0251969.
2000US-0251999.
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2000US-0249245.

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                                                                Score 18; pred. No.
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Search completed: January 31, 2003, 03:49:09 Job time: 287 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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## SUMMARIES

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	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX245292	VECCUT T
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D., Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,	Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D.,	1 (bases 1 to 378)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.		AX245292.1 GI:15859966	AX245292	Sequence 222 from Patent WO0166753.	AX245292 378 bp DNA linear PAT 28-SEP-2001		

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Stache-Crain,B.
Human genes and gene expression products
Patent: WO 0166753-A 222 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
1. 378
                                                                                                                                  1 (bases 1 to 322)
Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D.,
Sudduth-Klinger, J., Reinhard, C., Randazzo, F., Kennedy, G.C.,
Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M
Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and
Stache-Crain, B.
                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AX245346
AX245346.1
AX245370
Sequence
AX245370
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                                                                                                                                                                                                                                                                                                                                                                            Human genes and gene expression products
Patent: WO 0166753-A 276 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
Location/Qualifiers
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Mammalia; Eutheria;
1 (bases 1 to 327)
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ilarity 100.0%;
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/db_xref="taxon:9606"
64 c 81 g 9
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            from
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                                                                                                                                                                                                                                                                               Score 238; DB 6; L
Pred. No. 3.2e-137;
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hes 0;
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Matches 232; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAAAACACCCAAGCCGGAGTCTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAATCA 290
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                                                                                                     Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 15, 2000 this sequence version replaced gi:7242336.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genes and gene expression products Patent: WO 0166753-A 300 13-SEP-2001; Chiron Corporation (US); Hyseq Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sudduth-Klinger, J., Reinhard, C., Randazzo, F., Kennedy, G.C., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M. Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and
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                  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Ems. EWBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA sequence from clone
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1. (bases 1_to 59231)
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http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                          Phillimore, B.
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/db_xref="taxon:9606"
63 c 76 g 8
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Pred. No. 1.8e-133;
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n clone RP1-278022 on
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IMPORTANT: This sequence is not the entire insert of clone
RP1-278022 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP4-697P8 is at 59132 in this sequence.
The true right end of clone RP5-1099D15 is at 100 in this sequence.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one MI3 subclone; and the
assembly was confirmed by restriction digest. RP1-278022 is from
the library RPCI-1 constructed by the group of Pleter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome appling Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //www.chori.org/bacpac/home.htm
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/note="Charlie4a repeat: matches 25.
7631. .7695
     /note="MIR repeat: matches 169.
complement(15295..15803)
                                                                                                                                                                                                          /note="L2 repeat: matches 2657. .2750 of consensus" 13719. .13813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2927. .2992
/note-"Alu repeat: matches 242. .307 of consensus"
                                                                                                                                                                                                                                                                                                                  12860.
                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(10684. .11081)
/note="match: GSS: Em:AQ662878"
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/chromosome="20"
                                                                                                                                                          /note="L2 repeat: matches 2195. .2293 of consensus"
13814. .14087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="13 copies 2 mer aa 96% conserved" complement(10684. .11081)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSq repeat: matches 1. .225 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 13. .81 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3880 .4411
/note="LIM4 repeat: matches 4015. .4580 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3019. .3635
/note="LIME2 repeat: matches 5541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 3. .241 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MER3 repeat: matches 6. .191 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER5A repeat: matches 9. .188 of consensus"
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                                                                               /note="L2 repeat:
                                                                                                                                                                                                                                                                                                                                                                                         note="38 copies 2 mer aa 72% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="L1MC4 repeat: matches 7117. .7739 of consensus"
                                                                                                                               'note="L1MA5 repeat: matches 6025.
                                                                                                                                                                                                                                                                                  note-"match: GSS: Em:AQ035618"
                                                                                                                                                                                                                                                                                                                                       note="L1MA9 repeat: matches 5545. .6278 of consensus"
                                                          .15067
                                                                                                                                                                                                                                                                                                                                                                                                                 11168
                                                                                  matches
                                                                                  2078.
                               .262 of consensus*
                                                                                  .2195 of consensus"
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/note="match:
15961. .16498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="34 copies 2 mer ga 79% conserved"
complement(19364. .19600)
/note="match: GSS: Em:AQ035738"
22132. .22242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 26. .230 of consensus"
18267. .18357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="LTR16C repeat: matches 1. .387 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSg repeat: matches 1.
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18691. .18717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                            /note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                    /note-"MER1B repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="LTR33 repeat: matches 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="MIR repeat: matches 50. .139 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LlME3A repeat: matches 5964. .6159 of consensus"
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                                                    note-"MIR repeat: matches 66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="L1MC4 repeat: matches 7430. .7849 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e="L1MC4 repeat: matches 7841. .7973 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e-"LTR33 repeat: matches 410.
                                                                                              e="MER5A repeat:
                                                                                                                                                                                                                                                  e="L2 repeat: matches 1809.
                                                                                                                                    e"MIR repeat: matches 191.
                                                                                                                                                                                                                                                                                                                          ** "AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 26069
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28970
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34938
                                                                              36273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IR repeat; matches 20. .142 of consensus" 28469
                    copies 2
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                    mer aa
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                                                                                                matches 7.
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                    81% conserved"
                                                        .225 of consensus
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nes 119; Conserv
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Graham, L., Grand-Pierre, N., Levine, R., Lieu, C., Liu, G., Limazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McPheeters, R., Diver, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stojanovic, N., Schraus, S., Schraus, T., Meneus, T., Tesfavo, S., Norman, T., Tesfavo, S., Norman, T., Tesfavo, S., Stojanovic, N., Stojanovic, N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 65118)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-609K10

Unpublished
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/note="MIR repeat: matches 200. .250 of consensus"
/nomplement(45503. .46337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(43484. .44004)
/note="match: GSS: Em:AQ800109"
44765. .44818
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38841. .39254
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/note="LlMA9 ı
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40380. .40675
/note="11uJo repeat: matches 1. .306 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluJo repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note-"L1MA9 repeat: matches 3735.
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5; Pred. No. 1.6e-62;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 4226.
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LOW-PASS SEQUENCE
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COMMENT

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Submitted (14-OCT-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1995-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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7597
8345
8446: gap of
8445
8446: gap of
100 bp
9199
9298: gap of
100 bp
10047: contig of 749 bp in length
10048
10147: gap of
10148
10902: contig of 755 bp in length
10903
11002: gap of
100 bp
11785: contig of 783 bp in length
100 bp
11785: contig of 783 bp in length
100 bp
11785: contig of 783 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  will be sequenced to completion. In the event
the record is updated, the accession number wi
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11785: contig or 751 bp in le
12736: gap of 100 bp
12736: gap of 100 bp
13503: contig of 751 bp in le
12736: gap of 100 bp
13503: contig of 767 bp in le
13503: contig of 754 bp in l
14357: contig of 754 bp in l
3 14457: gap of 100 bp
8 15208: contig of 751 bp in l
3 14457: gap of 100 bp
16126: contig of 718 bp in l
7 16126: contig of 718 bp in l
7 16126: gap of 100 bp
17 16367: contig of 741 bp in l
88 16967: gap of 100 bp
18 17697: contig of 730 bp in l
98 17797: gap of 100 bp
18 18338: contig of 741 bp in l
98 17797: gap of 100 bp
18 18338: contig of 741 bp in l
98 17797: gap of 100 bp
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4145:
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8344:
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contig of 708
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contig of 732 bp in length
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contig of 748 bp in length
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contig of 732 bp in
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of 746 bp in
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22791 22890:
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27016: contig of .
7116: gap of 1:
27881: contig of .
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21101: contig of 7
201: gap of 10
21932: contig of 7
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49884; cc
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28747: contig of
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26169: contig of
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24480: contig of
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100 bp
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contig of 763 bp
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of 750 bp in length
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of 739 bp in
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                                                                                                                corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL451145 65811 bp DNA 1: Human DNA sequence from clone RP11-164A17 on
                                                                                                                                                                                                                                                                                                                                                                                                                          requests: clonerequest@sanger.ac.uk
on Jun 11, 2001 this sequence version replaced gi:14268205.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire. CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mappi
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                                                                                                database can be found at
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53350 54084: contig of 735 bp in length
54085 54184: gap of 100 bp
54185 54930: contig of 746 bp in length
54931 55030: gap of 100 bp
55031 55767: contig of 737 bp in length
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50838 51565: config of 728 bp in
51566 5165: gap of 100 bp
51666 52397: config of 732 bp in
52398 52497: gap of 100 bp
52498 53249: config of 752 bp in
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55768 55867: gap of 100 bp

55868 56655: contig of 788 bp in length

56556 56755: gap of 100 bp

56756 57500: contig of 745 bp in length

57501 57600: gap of 100 bp

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58458 59200; contig of 743 b
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RP11-164A17 is from the library RPCI-11.1 constructed by the group of Pleter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is not the entire insert of clone RP11-164A17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP3-365019 is at 65712 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.chor1.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            true right end of clone RP11-545I5 is at 100 in this sequence
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/note="match: GSS: Em:AQ744388"
complement(1. .100)
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/note="MER58A repeat: matches 2.
11397. .11750
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/note="MER2 repeat: matches 2.
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                                                                                                                                             /note="LIMEc repeat: matches 1778.complement(12258...12657)
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/note="MER46A repeat: matches 1.
10814. .11006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(6757
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/db_xref="taxon:9606"
/chromosome="6"
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                                                 complement (19964.
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13512. .13792
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                 /note-"match: 20006. .20049
/note="22
                                                                    /note="match: GSS:
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                                                                                                                                                                                                                                                           note="L1MEc repeat: matches 1201. .1743 of consensus"
                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ076115"
                                                                                                                                                                                                                                                                                                                                                                    /note="88 copies 2 mer ta 61% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match: GSS: Em:B33281"
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copies 2
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mer at 77% conserved"
                                  Em: AQ244751"
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/note="match: GSS: Em:AQ067991"
complement(21112 . 21482)
                                       /note="LIMEC repeat: matches 1778, 53511. .55046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="14 copies 2 mer ac 100% conserved" 22125. .22222
/note="LIME1 repeat: matches 4512.
55395. .55441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39379. .39450
                                                                                        /note="L1MEc repeat: matches 1026. .1669 of consensus"
53172. .53433
                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:AQ182459"
12825. .43364
                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluJo repeat: matches 73.
complement(42379 . .42834)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L2 repeat: matches 2668. .2737 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"L2 repeat: matches 2699.
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35192. .35325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 1992. .2327 of consensus"
34804. .35175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="Alusx repeat: matches 5. .305 of consensus"
34130. .34477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluJo repeat: matches 3. .300 of consensus"
33714. .34013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSq repeat: matches 1. .313 of consensus"
31232. .31427
/note="AluJo repeat: matches 140. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="15 copies 2 mer tg 86% conserved"
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25348. .25438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="MER5A repeat:
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23742. .23817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note-"L2 repeat: matches 2608. .2677 of consensus"
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21335. .21403
                                                                                                                                                    note="L2 repeat: matches 2254. .2534 of consensus"
                                                                                                                                                                                                                     'note="L2 repeat: matches 2355. .2522 of consensus"
0450. .50597
                                                                                                                                                                                                                                                                 'note="L1PB3 repeat: matches 5461. .6146 of consensus"
17303. .47470
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                                                                                                                                                                                                note="MIR repeat:
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                                                                                                                                                                                                matches 58. .207 of consensus"
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Homo sapiens genomic DNA, chromosome
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                         and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa
(E-mail:hattoriégsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 100403)
1attori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-JAN-2001) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete sequences.
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55442. .55564
/note="MER7C repeat: matches 1. .118 of consensus"
55565. .55869
/note="Alux repeat: matches 1. .303 of consensus"
55870. .56324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MER1B repeat: matches 1.
57945. .58113
                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
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57535. .57884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLT1H repeat: matches 32. .150 of consensus"
57330. .57429
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The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the places is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplanitae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                AP005251 129591 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome OSJNBb0011H15, *** SEQUENCING IN PROGRESS ***, in
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Submitted (15-AUG-2001) Takuji Sasaki, National Institute of
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                                               Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/cultivar="Nipponbare"
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/chromosome="8"
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NOTE: It currently consists of l contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence.

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Published Only in Database (2002)
2 (bases 1 to 129591)
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Submitted (20-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Aug 22, 2002 this sequence version replaced gi:21911559.
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
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                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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27555 c 28367 g 37453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome x, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
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Homo sapiens BAC clone CTB-119C2 from 7pl5, complete sequence.
ACO04520
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Direct Submission
Submitted (21-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                     Direct Submission
Submitted (03-FEB-2000)
University, 4444 Forest
5 (bases 1 to 132557)
                                                                                                                                                                                               Waterston,R.
Direct Submission
Submitted (01-APR-1998) Department of Genetics, Washington
Submitted (01-APR-1998) Pepartment of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 132557)
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Dubuque,T., Smith,A., Elliott
The sequence of Homo sapiens
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/db_xref-"taxon:9606"
/chromosome-"X"
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Pred. No.
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                                                                                                            Department of Genetics,
Park Avenue, St. Louis,
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Missouri 63108, USA
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Pocas

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COMMENT
                                                                                                                                                                                        On Feb 21, 2002 this sequence version replaced g1:3004572.
                         web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_RG119C02
                                                                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                     ----- Genome Center
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. all regions were double stranded, This sequence was finished as follows unless otherwise noted: sequenced with an alternate

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send Clone CTB-119C2 is from the first release of the human BAC library CITB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996), This clone is available from Research Genetics, Inc. MAPPING INFORMATION: (http://www.resgen.com). VECTOR: pBeloBAC11 SOURCE INFORMATION: mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc

source Actual start of this clone is at base position 1 of CTB-119C2; actual end is at base position 132572 of CTB-119C2.

Location/Qualifiers NEIGHBORING SEQUENCE INFORMATION: Selection: /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="7" /clone="CTB-119C2" /clone\_lib-"CITB-978SK-B" chloramphenicol .132557

FEATURES

repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region

/rpt\_family="MIR" 3975. .4300

:\_family-"Alu"

/rpt\_family="L2" 2792. .2967

rpt\_family-"L2"

.3454

rpt\_family-"Alu"

. 262

/rpt\_family="L2" 2067. .2202 /rpt\_family="Mariner"
571. .607 /rpt\_family="Alu" 465. .554

rpt\_family="L2"

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8272. .8569
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7954. .8040
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6937. 7144
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13943. .14241
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14463. .14687
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JOURNAL
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TITLE
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AUTHORS
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ORGANISM
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AC046149/c
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                   COMMENT
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Matches 20; Conserv
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Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
    Submitted (13 APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced gi:11094642.
                                                                                                      Worley, K.C.
Direct Submission
                                                                                                                                                                                          Muzny,D.M., Rives,M., Worley,K. and Gibbs,R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus 1 (bases 1 to 156469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACO46149 DNA linear HTG 16-OCT-2001 Mus musculus chromosome 10 clone RP23-310B11, WORKING DRAFT SEQUENCE, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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Genome Center
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0,

Center code: BCM

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-helpbbcm.tmc.edu

Contact: project Information Center: Baylor College of Medicine

Anderson, M.,

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FEATURES
                                                                                                                                                                          RESULT 14
AC009295/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
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                                  VERSION
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NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                109-108 bp DNA linear ROD 01-AUG: Mus musculus chromosome 10, clone RP21-39C4, complete sequence AC009295
AC009295.14 GI:9280781
HTG.
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Chemistry: Dye-primer Bodipy: 100% of reads
Chemistry: Dye-primer Bodipy: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 145589 bases at least Q40
Consensus quality: 154088 bases at least Q30
Consensus quality: 157075 bases at least Q20
Consensus quality: 157075 bases at least Q20
Consensus quality: 157075 bases; at least Q20
Consensus quality: 157075 bases; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.9x in Q20 bases; sum-of-contigs estimation
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38403 c 38896 g 38948 t
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/chromosome="10"
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5: contig of 11985 bp in length
5: gap of unknown length
7: contig of 11156 bp in length
7: gap of unknown length
7: contig of 9668 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Seren, B., Linton, L., Barna, N., Beckerly, R., Benn, J., Brown, A., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Baker, J., Baldwin, J., Barna, N., Collins, S., Collymore, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Kann, L., Funke, R., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Funke, R., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Meddrin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Maylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Paylin, B., Naylor, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus chromosome 10, clone RP21-39C4
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-AUG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 19, 2000 this sequence version replaced gi:8571747. All repeats were identified using RepeatMasKer: Smit, A.F.A. & Green, P. (1996-1997) Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                            Center project name: L760 Center clone name: 39_C_4
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                              /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                     /clone="RP21-39C4"
/clone_11b="RPCI-21 Female Mouse PAC"
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Snoo

repeat\_region

repeat\_region

/rpt\_family-"FLAM\_A" 7581. .7618

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(CA)n

repeat\_region repeat\_region repeat\_region

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15475

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complement(15532. .156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(7061. .7239)
/rpt_fam1ly-"AluJo"
complement(7448. .7557)
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11048. .11067
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complement(31814..32710)
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                                                                                                                                                                                                                family-"AT_rich"
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                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                              RESULT 15
AC119775/c
LOCUS
                                                                                                                                                                                                                                    Db 105501 TCCCGGGAAGGAAGGTACCA 105482
                                                                                                                   ACCESSION
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 REFERENCE
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Best Local Similarity
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                                                                                   AC119775 162394 bp DNP
RATTUS norvegicus clone CH230-464J18,
***, 61 unordered pieces.
AC119775
AC119775.4 GI:21747184
HTG: HTGS_PHASE1.
                        Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
(bases 1 to 162394)
                                                                                                                                                                                                                                                                                          5.3%; Score 20;
nilarity 100.0%; Pred. No.
Conservative 0; Mismatci
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                                                                                                                                                                                                                                                                                                                                                                   complement(54449...54619)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _family="AluJo"
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. .38803
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                                                                                                                                                                                                                                                                                                                                                                                                                                              family="(CCAA)n"
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repeat\_region

family-"FRAM"

family-"CT-rich"

repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region

\_fami

lly-"(TGG)n"

family-"(GA)n"

. .20528 family-

repeat\_region repeat\_region

family-"Alus"

family="(TG)n" . .28877 family-"MIR" tamily-

.y="(CA)n" 197

family-

"(GA)n"

family-"(TG)n" family-"L1MB2" family

"AluJo"

family="(TG)n"

NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.

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REFERENCE
AUTHORS
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Worley,K.C.
Direct Submission
Submitted (02-MAY-2002) Human Genome Sequencing Center, Department Submitted (02-MAY-2002) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:20467838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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* NOTE: Estimated insert size may differ from sequence length 
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
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                                                                                                           Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 104933 bases at least Q40
Consensus quality: 112584 bases at least Q30
Consensus quality: 117408 bases at least Q20
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Sequence 23, Appl Sequence 27, Appl Sequence 27, Appl Sequence 289, App Sequence 589, App Sequence 587, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 952, App Sequence 103, App Sequence 102, App Sequence 104, App Sequence 6004, App Sequence 6004, App Sequence 6004, App Sequence 60035, App Sequence 60035, App Sequence 60010, A
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	Sequence 3839, Ap		Sequence 41, Appl	٠ - ن		Sequence 131, App					) N		Sequence 37524, A	Sequence 37523, A	Sequence 3/523, A		1109	1109	Sequence 5980, Ap

## ALIGNMENTS

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CURRENT CURRENT PRIOR AI PRIOR AI PRIOR FI PRIOR EI PRIOR AI	APPLICANT APPLIC	PCT-US02-10366-23 Sequence 23, Ap GENERAL INFORMA APPLICANT: Pad APPLICANT: Sh APPLICANT: Ra APPLICANT: Ra APPLICANT: Me APPLICANT: Me APPLICANT: Me
NT APPLICATION NT FILING DATE APPLICATION FILING DATE: APPLICATION I	THE STATE OF THE S	SULT 1  T-US02-10366-23  Sequence 23, Applica  GENERAL INFORMATION:  APPLICANT: Padigaru  APPLICANT: Shenoy,  APPLICANT: Kekuda,  APPLICANT: Rastell  APPLICANT: Mezes,  APPLICANT: Smithso
NT EFERENCE: 21402 5267 002 NT EFILING DATE: 2002-04-0 APPLICATION NUMBER: 10/1 FILING DATE: 2002-04-0 FILING DATE: 2002-04-02 APPLICATION NUMBER: 60/2 APPLICATION NUMBER: 60/2 APPLICATION NUMBER: 60/2 FILING DATE: 2001-04-05 APPLICATION NUMBER: 60/2 FILING DATE: 2001-04-06 APPLICATION NUMBER: 60/2 FILING DATE: 2001-04-10 APPLICATION NUMBER: 60/2 FILING DATE: 2001-04-10 APPLICATION NUMBER: 60/2	Gul, Aladyla Gerlach, Valerie Casman, Stacie Boldog, Ferenc Li, Li Zerhusen, Bryan Tchernev, Veliza Gangolli, Esha Vernet, Corine Spytek, Kimberly Malyankar, Uriel Patturajan, Meer Miller, Charles Taupier, Raymond Heyes, Melvyn Ju, Jingfang Peyman, John Catterton, Elina MacDougall, John Edinger, Shlomit Stone, David Mazur, Ann INVENTION: NOVEL AN	Application PC Application PC RMATION: Padigaru, Mural Shenoy, Suresh Kekuda, Ramesh Kekuda, Ramesh Rastelli, Luca Mezes, Peter Smithson, Glan
N NUMBER: PCT/ NE: 2002-04-03 NUMBER: 10/210 2002-04-02 NUMBER: 60/281 2001-04-03 NUMBER: 60/281 2001-04-05 NUMBER: 60/282 2001-04-06 NUMBER: 60/282 2001-04-06 NUMBER: 60/282 2001-04-06 NUMBER: 60/282 2001-04-10 NUMBER: 60/283	Valeritacie erenc Veliz Esha orine imber: harle; ha	ition PC/TUS02  Muralidhara Suresh Ramesh LL Luca Peter Peter Potlanda
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PRIOR FILING DATE: 2001-04-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 251
SEQ ID NO 23
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Best Local Similarity 53.7%;
Matches 73; Conservative
                                                                                    APPLICANT:
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              APPLICANT: Mazur, Ann TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, TITLE OF INVENTION: NUCLEIC THE ANTIGENS, AND METHODS OF USE TITLE OF INVENTION: ACIDS ENCODING THE ANTIGENS, AND METHODS OF USE
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TYPE: DNA
ORGANISM: Homo sapiens
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DR FILING DATE: 2001-04-12
DR APPLICATION NUMBER: 60/283657
DR FILING DATE: 2001-04-13
DR APPLICATION NUMBER: 60/283710
DR FILING DATE: 2001-04-13
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REFERENCE: 21402-322A-061
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MacDougall, John
Edinger, Shlomit
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Patturajan, Meera
Miller, Charles
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Tchernev, Velizar
Gangolli, Esha
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Guo, Xiaojia
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Kekuda, Ramesh
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                                                                                    Stone, David
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                                                                                                                                                          John
           NUCLEIC ACIDS ENCODING THE ANTIGENS,
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Pred. No. 0.34;
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PCT-US02-10366-27
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APPLICANT:
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PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/281086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281906
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CURRENT FILING DATE: 2002-04-03
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PRIOR APPLICATION NUMBER: 60/282020
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                    APPLICANT
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OR APPLICATION NUMBER: 60/282930
OR FILING DATE: 2001-04-10
OR APPLICATION NUMBER: 60/283512
OR FILING DATE: 2001-04-12
OR APPLICATION NUMBER: 60/283444
OR FILING DATE: 2001-04-12
OR APPLICATION NUMBER: 60/283657
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OR FILING DATE: 2001-04-13
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Similarity 53.7%;
             Vernet, Corine
Spytek, Kimberly
Malyankar, Uriel
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Kekuda, Ramesh
Rastelli, Luca
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                                                                  Gangolli, Esha
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Casman, Stacie
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Guo, Xiaojia
                                                                                    Tcherney,
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Patturajan, Meera
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Guo,

Xiaojia

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(1791)
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NUMBER OF SEQ ID NOS: 251
SEQ ID NO 27
LENGTH: 2067
                                                      Sequence 25, Application PC/TUS0210366
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
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CURRENT APPLICATION NUMBER: PCT/US02/10366
CURRENT FILING DATE: 2002-04-03
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PRIOR APPLICATION NUMBER: 60/281086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281906
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
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PRIOR APPLICATION NUMBER: 60/282020
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282930
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
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PRIOR APPLICATION NUMBER: 60/283444
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283657
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
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Local Similarity 53.7%;
les 73; Conservative
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MacDougall, John
Edinger, Shlomit
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Mezes, Peter
Smithson, Glennda
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                                           Luca
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CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: PCT/US02/10366
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 10/214153
PRIOR FILING DATE: 2002-04-02
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281906
PRIOR APPLICATION NUMBER: 60/282020
PRIOR APPLICATION NUMBER: 60/282020
PRIOR APPLICATION NUMBER: 60/282020
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-06
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PCT-US02-10366-25
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; NUMBER OF SEQ ID N
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Best Local S
Matches 73
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TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE ANTIGENS, AND METHODS OF USE
FILE REFERENCE: 21402-322A-061
FILE REFERENCE: 21402-322A-061
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PRIOR FILING DATE: 2001-04-12
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                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (31
                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                    1152 ATATAATGTACTGATTTTAACAATGCAGGCCTCACTGCCAAAAGTTCTTCGGTTTTGTGC
                                                                                                                                1092 TGGAACCTCTACGCTCTTGGTTTGGGTTGGAGTCATCAGATACCTGGGTTATTTCCAGGC 1151
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DR FILING DATE: 2001-04-12
DR APPLICATION NUMBER: 60/283657
DR FILING DATE: 2001-04-13
DR APPLICATION NUMBER: 60/283710
DR FILING DATE: 2001-04-13
211 TCAACATGCTTTGACT 226
                                                                                                                                                                91 TIGAATGTGTGTTCTGGAGGTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCCGTT 150
                                                                                                                                                                                                               Local Similarity 53.7 tosal Similarity 53.7
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                                                                                 GTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGC 210
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Spytek, Kimberly
Malyankar, Uriel
Patturajan, Meera
Miller, Charles
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Casman, Stacie
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MacDougall, John
Edinger, Shlomit
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                                                                                                                                                                                                                                    Score 35.2; DB 1;
Pred. No. 0.37;
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                     63;
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1212 TTGTGCTGGTATGATT 1227

US-10-276-774-299

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US-10-276-774-299
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                                                                                                  CURRENT APPLICATION NUMBER: PCT/US02/38526
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: PCT/US00/34263
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-26
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Best Local Similarity 52.9
72; Conservative
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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CURRENT FILING DATE: 2002-11-18
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APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Chongjun
APPLICANT: Mulero, Julio J
APPLICANT: Boyle, Bryan J.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUCI
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                                                       APPLICATION NUMBER: US 09/496,914 FILING DATE: 2000-02-03
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                                   CATION NUMBER: US 09/560,875
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PCT/US01/03800
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Best Local Similarity
Watches 72; Conserve
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PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: PCT/US00/34263
PRIOR APPLICATION NUMBER: PCT/US00/34263
PRIOR FILING DATE: 2000-12-26
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SOFTWARE: PatentIn
SEQ ID NO 587
LENGTH: 1640
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PRIOR APPLICATION NUMBER: US 09/598,075
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APPLICANT: Boyle, Bryan J.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POI
FILE REFERENCE: HYS-B1/PCT
CURRENT APPLICATION NUMBER: PCT/US02/38526
CURRENT FILING DATE: 2002-12-03
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                                                                  NUMBER OF SEQ ID NOS:
                                                                                    Remaining Prior Application data removed
                                                                                                             PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/US01/04098
PRIOR FILING DATE: 2001-02-05
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APPLICATION NUMBER: US 09/560,875
                                                                                                                                                                       FILING DATE: 2000-04-27
APPLICATION NUMBER: PCT/US01/03800
FILING DATE: 2001-02-05
APPLICATION NUMBER: US 09/598,075
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Zhao, Qing
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Wang, Jian-Rui
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Query Match
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Thes 72; Conserve
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                                                                                                                                                               RESULT 9
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SEQ ID NO 33882
LENGTH: 158
                                                                                                              Sequence 7, Application PC/TUS0232700 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
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                                                               APPLICANT:
                                                                                APPLICANT:
                                                                                              APPLICANT: Keith, Tim
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LOCATION: (1)..(1629)
OTHER INFORMATION:
                                                APPLICANT:
                                 APPLICANT:
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   INVENTION:
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             Van Eerdewegh, Paul
Dupuis, Josee
Del Mastro, Richard (
Allen, Kristina
                                                                                Little, Randall D.
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NUCLEOTIDE AND AMINO ACID SEQUENCES
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53.4%;
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                                 Richard G.
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Pred. No. 1.1;
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Pred. No. 0.6;
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US-10-271-416-7
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ: ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence /, Application GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                           SOFTWARE:
SEQ ID NO 7
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Best Local Similarity
                                     Matches. 104;
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                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/271,416
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/328,424
PRIOR FILING DATE: 2001-10-11
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NAME/KEY: misc_feature
LOCATION: (1)...(45450)

OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES ATTITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES A
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Keith, Tim
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                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(45450)
OTHER INFORMATION: n =
                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                             LENGTH: 45450
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 133 CCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAG 192
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Del Mastro, Ri
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                                   Score 32.6; DB pred. No. 6.7; O; Mismatches
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Pred. No. 6.
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                                                                     DB 6;
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SEQ ID NO 5935

LENGTH: 334

TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: jC-gmf102220076bl1a1
US-09-531-113-5935
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                                                           Sequence 952, Application US/09950084

GENERAL INFORMATION:
GEORGE H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/10963US2
CURRENT APPLICATION NUMBER: US/09/950,084
CURRENT FILING DATE: 2001-09-10
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TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION NUMBER: US/09/531,113
CURRENT FILING DATE: 2000-03-22
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                   PRIOR FILING DATE: 1999-10-14
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      APPLICATION NUMBER:
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US 09/353,718
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NAME/KEY: misc_feature; LOCATION: 388; OTHER INFORMATION: n=a, US-09-513-999C-30304
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; Sequence 30304, Application US/09513999C
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SEQ ID NO 952
LENGTH: 264
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Matches
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SEQ ID NO 30304
LENGTH: 410
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                                                                       Query Match
                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
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                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: 387
OTHER INFORMATION: v-a
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                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                         TYPE: DNA
196 TACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGA 255
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                                                      Local Similarity
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les 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-03-10 APPLICATION NUMBER: US 09/036,720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/266,555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/266,557
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                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application data removed - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-03-1
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Pred. No. 1.7;
                                                      Score 32;
Pred. No.
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                                  Mismatches
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                                                        2.3;
                                                                      DB 5;
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390 TANBTACTCTCATTCTCAAAAGCCAGGCATTCATAAATGTGGAGCTATGTCTTTTTCTGA 331

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APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: Sleath, Paul R.

APPLICANT: Sleath, Paul R.

APPLICANT: McNeill, Patricia D.

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

FILE REFERENCE: 210121.426C12

CURRENT APPLICATION NUMBER: US/10/294,443

CURRENT APPLICATION NUMBER: US/10/294,443

NUMBER OF SEQ ID NOS: 243

NUMBER OF SEQ ID NOS: 243

NUMBER OF SEQ ID NOS: 243

SECOTOMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : NUMBER OF SEQ ID NOS: 243
: SOFTWARE: FastSEQ for Windows Version 3.0
: SEQ ID NO 103
: LENGTH: 2966
: TYPE: DNA
: ORGANISM: Babesia microti
US-10-294-443-103
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US-10-294-443-103
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                 SEQ ID NO 112
LENGTH: 3011
TYPE: DNA
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Best Local S
Matches 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Secrist, Heather AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: COMPOUNDS AND TREATMENT OF B. MICROTI INFECTION FILE REFERENCE: 210121.426C12
CURRENT APPLICATION NUMBER: US/10/294,443
CURRENT FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                             Sequence 112, Application US/10294443 GENERAL INFORMATION:
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ORGANISM: Babesia microti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 TAGCAGAAGTCTT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 TGGTAMAGTTCAGGATTTACTAATTGGTACAATCAGAGAGCACTGGTTTCGAGGCTGCTG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 AGGGATGGTGATGGAAGTGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 GATGATATACATGAATATGCAT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 GGTGATGGAGATGCCAATCCAT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 TATTCTACTTTTAATATATATTTTTATTCAATAATATACTCTTTCATATTTTGTACTAT 330
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Local Similarity 51.4%;
les 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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US-10-294-443-112
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Best Local Similarity 51.4
Matches 73; Conservative
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                                                                                                                                   271 TATTCTACTTTTAATATAATTTTTTTATTCAATAATATACTCTTTCATATTTTGTACTAT 330
391 GATGATATACATGAATATGCAT 412
                          262 GGTGATGGAGATGCCAATCCAT 283
                                                                 331 TTTATATAATCATATATATATATATATATATATTTGATAATTGAATATATATCAATAAT 390
                                                                                                202 GTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT 261
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                                                                                                                                                                                                                                    DB 6; Length 3011;
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Search completed: January 31, 2003, 01:19:25 Job time : 239 secs

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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378
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/cgn2_6/ptcdata/1/pna/US094_COMB.seq:*
/cgn2_6/ptcdata/1/pna/US095A_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US085_COMB.seq:*
/cgn2_6/ptodata/1/pna/US086_COMB.seq:*
/cgn2_6/ptodata/1/pna/US087_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US089_COMB.seq:*
/cgn2_6/ptodata/1/pna/US090_COMB.seq:*
/cgn2_6/ptodata/1/pna/US091_COMB.seq:*
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47: /cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
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49: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
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56: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
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64: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
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77: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
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79: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
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79: /cgn2_6/ptodata/1/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Query Match	Query Match Length D	BG	ID	Description
_	378	100.0	378	<u>ω</u>	US-09-803-719-222	Sequence
N I	342	90.5	512	24	-09-621-	Sequence
ωı	342	90.5	512	32	US-09-834-366-8066	Sequence
4 (	342	90.5	512	5	US-60-147-499-3594	Sequence
י וט	342	90.5	512	<u>σ</u>	US-60-197-873-8066	Sequence
on (	299.6	79.3	327	3	US-09-803-719-276	Sequence
7	279.6	74.0	322	3	US-09-803-719-295	Sequence
<b>3</b> 0 ·	275	72.8	318	31	US-09-803-719-300	Sequence
9	226.8	60.0	562	28	US-09-718-457-565	Sequence
10	131	34.7	403	20	US-09-534-844A-5172	Sequence
c 11	83.4	22.1	524	27	US-09-689-907-861	Sequence
c 12	79.4	21.0	806	39	US-10-098-754-19036	Sequence
13	75.6	20.0	125	27	US-09-685-045-1053	Sequence
14	48.8	12.9	381	17	US-09-362-510-51216	Sequence
15		12.9	381	17	US-09-362-510A-51216	Sequence
16		12.9	381	34	US-09-904-013-51216	Sequence
17	40.2	10.6	453	17	US-09-306-350A-28514	Sequence
18	40.2	10.6	453	ω <b>4</b>	US-09-909-629-28514	Sequence
19	39.8	10.5	613	25	US-09-652-123-5950	Seguence
	39.2	10.4	1266	19	US-09-505-532-14754	Sequence
21	39.2	10.4	1266		US-09-819-091A-14754	Sequence

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APPLICANT: WILLIAMS, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Innis, Michael A.
APPLICANT: Innis, Michael A.
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Reinhard, Christoph
APPLICANT: Randazzo, Filippo
APPLICANT: Randazzo, Filippo
APPLICANT: Kennedy, Giulia C.
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Lamson, George
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Labat, Tyan
APPLICANT: Labat, Tyan
APPLICANT: Labat, Tyan
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATON NUMBER: US/09/803,719
CURRENT FILING DATE: 2000-03-09
PRIOR APPLICATON NUMBER: US/09/803,719
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 222
LENGTH: 378
TWONDOWNERS: MICHAEL STANDOWNERS SOFTMARE: FastSEQ for Windows Version 4.0
                                                    ; LENGTH: 378
; TYPE: DNA
; ORGANISM: HOMO &
US-09-803-719-222
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-09-803-719-222
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 222, Application US/09803719 GENERAL INFORMATION:
          Query Match
Best Local Similarity
Matches 378; Conserv
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                                                              sapiens
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                    100.0%;
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20 US-09-534-859-363
31 US-09-552-086-14635
22 US-09-552-086-14635
23 US-09-874-708A-83442
53 US-09-874-708A-83442
53 US-09-874-708A-83442
54 US-09-874-708A-82309
1 PCT-US01-10366-23
1 PCT-US01-10366-27
1 PCT-US01-10366-27
1 PCT-US01-10366-27
1 US-10-114-153-27
1 US-10-114-153-25
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           0;
        Score 378; DB 31, Pred. No. 3.8e-106;
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                              Length
           Indels
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Sequence 363, App
Sequence 14635, A
Sequence 823042, A
Sequence 8230, Appl
Sequence 23, Appl
Sequence 21, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 256549,
Sequence 256549,
Sequence 30211, A
Sequence 96308, Ap
Sequence 96308, Ap
Sequence 96308, Ap
Sequence 96308, Ap
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3594
LENGTH: 512
TYPE: DNA
ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: 84..404
US-09-621-976-3594
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US-09-621-976-3594
; Sequence 3594, Application US/09621976
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                           Best
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                     Query Match
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           GGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGCAGAAGTCT
                                                                                                                AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCC
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                              TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTTGGCACACATTGAAGGGATGGTGAT
Conservative
                                                                                                                                                                                                           90.5%;
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                                                                                                                                                                                                Score 342; DB 24;
Pred. No. 6.3e-95;
0; Mismatches 5;
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CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: PALENT.pm
SEQ ID NO 8066
LENGTH: 512
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US-09-834-366-8066
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Sequence 3594, Application US/60147499
; Sequence 3594, Application US/60147499
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Properties File Reference: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/60/147,499
; CURRENT FILING DATE: 1999-08-05
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US-09-834-366-8066
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US-60-147-499-3594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.5%; pest Local Similarity 98.6%; Matches 345; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean Yves
TITLE OF INVENTION: ESTs and Encoded Human Proi
FILE REFERENCE: 81.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                    TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                        AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTCC 147
                                                                                                                                                                             TCTTGGCAAAGATTCCTCCAGGGAAGGAAGGTACCATTGGAGAACCATGC
                                                                                                                                                                                         TCTTGGCAAAGATTCCTCCCGGGAAGGAAGGTACCATTGGAGAACCATGC 377
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Pred. No. 6.3e-95;
0; Mismatches 5;
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; NAME/KEY: CDS
; LOCATION: 84..404
US-60-147-499-3594
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SOFTWARE: Patent.pm
SEQ ID NO 3594
LENGTH: 512
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; LOCATION: 84..404
US-60-197-873-8066
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GENERAL INFORMATION:
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Best Local S
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SOFTWARE: Patent.pm
SEQ ID NO 8066
LENGTH: 512
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APPLICANT:
APPLICANT:
                                                                                       Query Match 90.5 Best Local Similarity 98.6 Matches 345; Conservative
                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 81.US1.PRO
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                              LENGTH: 512
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                    FEATURE:
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Tanaka, Hiroaki
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CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                       APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: ESTs and Encoded Human Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 GAATGACGCAGCACCTCTGAGAGGAACATAAGGAAACACCCAAGCCGGAGTCTCTCACA 76
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                          AGCTTGAATGTGTGTGTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCC 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTGGCAAAGATTCCTCCAGGGAAGGAAGGTACCATTGGAGAACCATGC
AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCC 147
                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards, Jean Baptiste
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Pred. No. 6.3e-95;
                                                                                     Score 342; DB 63; pred. No. 6.3e-95; 0; Mismatches 5;
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CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: FBStSEQ for Windows Version 4.0
SEQ ID NO 276
CEQ ID NO 276
LENGTH: 327
TYPE: DNA
ORGANISM: Homo sapiens
US-09-803-719-276
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APPLICANT:
APPLICANT:
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APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
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                                                                                                                                                                                 Local
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                                                                                                    GAATGACGCAGCTCTGAGAGGAACATAAGGAAAACACCCCAAGCCGGAGTCTCTCACA 80
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                                                                  AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCC 147
                                   AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCC 140
                                                                                                                                                                  302;
                                                                                                                                                                               h 79.3%;
Similarity 98.7%;
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Dickson, Mark
Drmanac, Snezana
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Kita, David
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Drmanac, Radoje
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Kennedy, Giulia C
Pot, David
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Sudduth-Klinger, Julie
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Pred. No. 7.5e-82;
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US-09-803-719-295
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LENGTH: 322
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APPLICANT:
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CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEO ID NOS: 2396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
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                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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                                                                                              Local Similarity
GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 207
                              AGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCC
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Leshkowitz, Dena
Kita, David
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Drmanac, Snezana
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Crkvenjakov, Radomir
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Kennedy, Giulia C.
Pot, David
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                                                                                                                                                                 Conservative
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98.6%;
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Pred. No. 1.:
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US-09-803-719-300
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SEQ ID NO 300
LENGTH: 318
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Best Local
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TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
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                                                                                      156 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 215
  268 GGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGT 310
                                                          208 TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT 267
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                               TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT 275
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Jones, Lee William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innis, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leshkowitz, Dena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lamson, George
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Altaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Snezana
                                                                                                                                                                                                                                                                           72.8%;
                                                                                                                                                                                                                                                            Score 275; DB 31;
Pred. No. 3.2e-74;
0; Mismatches 5,
                                                                                                                                                                                                                                                                                         Length 318;
                                                                                                                                                                                                                                                              Indels
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Query Match
Best Local Similarity
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APPLICANT: Wattler, Sigrid
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Polynucleotides and
CURRENT APPLICATION NUMBER: US/09/718,457
CURRENT APPLICATION NUMBER: US 60/167,870
PRIOR APPLICATION NUMBER: US 60/167,870
FINDER: OF SEQ ID NOS: 1008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 565
LENGTH: 562
TYPE: DNA
ORGANISM: Homo sapiens
US-09-718-457-565
                                                                                       ; ORGANISM: Homo sapiens US-09-534-844A-5172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-534-844A-5172
                                                                                                                                             SOFTWARE: Hy-patent.pl Version 1.1
SEQ ID NO 5172
LENCTH: 403
TYPE: DNA
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Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dramanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birg:
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee W.
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various CDNA Libraries FILE REFERENCE: 21272-109 (775) CURRENT APPLICATION NUMBER: US/09/534,844A CURRENT FILING DATE: 2001-03-24 PRIOR APPLICATION NUMBER: 60/126,605 PRIOR FILING DATE: 1999-03-26
                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTAGTACTTGGTTTTA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 TCTTGGCAAAGATTCCTCCCGGGAAGGAAGGTACCATTGGAGAACCATGC 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGATGCCAATCCATGGAATCAGGTGGCACAGCTATGTTGGTAGCTATAGCAGAAGTCT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stache-Crain, Birgit
Dickson, Mark C.
Jones, Lee W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%;
   34.78;
95.78;
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Pred. No. 3.5e-59;
Score 131; DB 20; Pred. No. 1.6e-29;
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APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Polynucleotides and the
TITLE OF INVENTION: Novel Human Polynucleotides and the
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: LEX-0064-USA
CURRENT APPLICATION NUMBER: US/09/689,907
CURRENT FILING.DATE: 2000-10-11
PRIOR APPLICATION NUMBER: US 60/158,799
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 861
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US-09-689-907-861/c
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                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 19036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                       APPLICANT: Ramachandran, Rakesh
TITLE OF INVENTION: NOVEL NUCLEIC AND PROTEIN HOMOLOGS
FILE REFERENCE: ATX-001CN
CURRENT APPLICATION NUMBER: US/10/098,754
CURRENT FILING:DATE: 2002-03-15
CURRENT FILING:DATE: 2002-03-15
                                                                                                                                                                                                                                                                                                                               APPLICANT: Harrington, John J
APPLICANT: Jackson, P. David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nehls, Michael
                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/791539 PRIOR FILING DATE: 2001-02-22
                                          LENGTH: 806
TYPE: DNA
                                                                                                                         NUMBER OF SEQ ID NOS: 21107
                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 524
TYPE: DNA
ORGANISM: homo sapiens
                         ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGATGCCAATCCATGGAATCAAGTGGCACAGCTATGTTGGT 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                            Sherf, Bruce A.
                                                                                                                                                                                                                                                                                           Cain, Scott
                                                                                                                                                                                                                                                                       Rundlett, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09689907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.1%;
llarity 98.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Application US/10098754
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Pred. No. 1e-14;
0; Mismatches 1;
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TITLE OF INVENTION: Novel Human Polynucleotides and TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: LEX-0055-USA
CURRENT APPLICATION NUMBER: US/09/685,045
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/158,741
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1053
LENGTH: 125
TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (1)...(806)
; OTHER INFORMATION: n =
US-10-098-754-19036
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, NAME/KEY: misc_feature
; LOCATION: (1)...(125)
; OTHER INFORMATION: n =
US-09-685-045-1053
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                                                                                                                                                             RESULT 14
US-09-362-510-51216
Sequence 51216, Application US/09362510
GENERAL INFORMATION:
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US-09-685-045-1053
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Matches
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Best Local Similarity
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362,510
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 09/221,820
EARLIER APPLICATION NUMBER: 1998-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 AAGTCTTCTTGGCAAAGATTC 343
                                                                                                                                                                                                                                                                                                                                                                                                                        322 AAGTCTTCTTGGCAAAGATTC 342
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es 103; Conserv
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                                                                                                                                                                                                                                                                                                                                                    GGNATGGTGATNGNGATGCCNNTCCANGGAATCANGGGGC-CNTCTATGNCCCTTGCTCT 119
                                                                                                                                                                                                                                                                                                                                                                                       GGGATGGTGATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTAT 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, T, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 75.6; D;
; Pred. No. 1.5e
0; Mismatches
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Pred. No. 2.2e-13;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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RESULT 15
US-09-362-510A-51216
Sequence 51216, Application US/09362510A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362,510A
CURRENT APPLICATION NUMBER: US 09/221,820
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 09/221,820
VAMBER OF SEQ ID NOS: 62165
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51216
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(381)
OTHER INFORMATION: n - A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / NVMBER OF SEQ ID NOS: 62165

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 51216

LENGTH: 381

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(381)
OTHER INFORMATION: n = A,T,C or G
US-09-362-510-51216
Search completed: January 31, 2003, 02:17:22 Job time: 3495 secs
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                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                       Matches
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Best Local Similarity 96.2%;
                                                             326 CTTCTTGGCAAAGATTCCTCCCGGGAAGGAAGGTACCATTGGAGAACCATGC 377
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                                                                                                                                    12.9%;
nilarity 96.2%;
Conservative
                                                                                                                                Score 48.8; DB 17;
Pred. No. 0.00049;
0; Mismatches 2;
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                                                                                                                                                                    Length 381;
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        seq
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length: 2000000000
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_FUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09_NEM_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEM_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEM_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEM_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEM_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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  9 US-09-938-842A-3096
10 US-09-737-178-103
10 US-09-737-178-112
9 US-09-286-488-10
10 US-09-737-178-10
10 US-09-737-178-10
10 US-09-736-692-4354
10 US-09-745-763-204
10 US-09-746-877-2678
10 US-09-746-877-2678
10 US-09-764-877-2678
10 US-09-764-877-1518
10 US-09-764-877-1518
10 US-09-764-877-1518
10 US-09-764-877-1518
10 US-09-764-877-1518
10 US-09-764-877-1518
10 US-09-764-877-1513
10 US-09-764-877-15145
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Sequence 3096, Ap
Sequence 112, Appl
Sequence 110, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 204, Appl
Sequence 204, Appl
Sequence 2678, App
Sequence 2678, Appl
Sequence 1518, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
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### ALIGNMENTS

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APPLICANT: Kreps, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIN)
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3996
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US-09-938-842A-3096
Sequence 3096, Application US/09938842A
Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                            US-09-938-842A-3096
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Best Local S
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
482 AGTTAAACGTAAAGCTTTATTAAACAAAGAACAAAT 517
                                       226 TGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT 261
                                                                                                                                                                               362 GGAGACCATATATGGACTTCTGGAACTCCGCTTAACATATCTCTCGTGTACACACATGCG 421
                                                                                                                                                                                                                         106 GGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTT 165
                                                                                                                                                                                                                                                                 y Match 10.4%;
Local Similarity 53.2%;
nes 83; Conservative
                                                                                      CTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGAC
                                                                                                                                                                                                                                                                   Score 39.2; DB 9;
Pred. No. 0.013;
0; Mismatches 73;
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US-09-737-178-103

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; SOFTWARE: FASTSEQ for Windc
; SEQ ID NO 112
; LENGTH: 3011
; TYPE: DNA
; ORGANISM: Babesia microti
US-09-737-178-112
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; SEQ ID NO 103

; LENGTH: 2966

; TYPE: DNA

; ORGANISM: Babesia microti

US-09-737-178-103:
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Patent No. US20010029295A1
GENERAL INFORMATION:
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Best Local S
                                         Query Match
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APPLICANT:
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APPLICANT:
   Matches
                                                                                                                                                                                     FILE REFERENCE: 210121.426C9
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEO ID NOS: 144
                                                                                                                                                                                                                                              APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 TTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTG 201
 Local Similarity 51.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 8.4%; Score 31.6; DB 10; Local Similarity 51.4%; Pred. No. 4.4; es 73; Conservative 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGATATACATGAATATGCAT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGATGGAGATGCCAATCCAT 283
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                                                                                                                                                                             FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                      Houghton, Raymond L. Sleath, Paul R.
                                                                                                                                                                                                                                                                                                                                McNeill, Patricia D. Homer, Mary
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Lodes, Michael J.
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                   8.4%; Score 31.6; D
51.4%; Pred. No. 4.4;
 0
   Mismatches
                                     DB 10;
   69;
                                   Length 3011;
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Gaps
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GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Sleath, Paul R.

APPLICANT: Sleath, Paul R.

APPLICANT: MCNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

FILE REFERENCE: 210121.426C3

CURRENT APPLICATION NUMBER: US/09/286,488

CURRENT FILING DATE: 1999-04-05

NUMBER OF SEQ ID NOS: 83
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; ORGANISM: Babesia microti
US-09-286-488-10
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                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Reed, St
APPLICANT: Lodes, M
APPLICANT: Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10 LENGTH: 3701
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 3.4
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09737178 Patent No. US20010029295A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.4%;
Best Local Similarity 51.4%;
Matches 73; Conservative
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Patent No. US20020169136A1
                                                                                                                          APPLICANT: Sleath, Paul R.
APPLICANT: MCNeill, Patricia D.
APPLICANT: HOMET, MATY
APPLICANT: Secrist, Heather
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1119 GATGATATACATGAATATGCAT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1059 TTTATATAATCATATATATATATATATATATATATATTTGATAATTGAATATATCAATAAT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 GGTGATGGAGATGCCAATCCAT 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 TTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 GTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT 261
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                                                                                                                                                                                                                                           Houghton, Raymond L. Sleath, Paul R. McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                        Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                 Reed, Steven G.
                           for Windows Version 3.0
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; TYPE: DNA
; ORGANISM: Babesia
US-09-737-178-10
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Patent No. US20020048763A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 73; Conserv
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/00670 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                               PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/00667 PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                                                                            FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00662
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Pred. No. 4.
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; Sequence 4354, Application US/09796692 publication No. US20020198362A1 ; GENERAL INFORMATION: APPLICANT: Gaiger, Alexander
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LENGTH: 568
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Best Local
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APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0241
CURRENT FILICATION NUMBER: US/10/002,344A
CURRENT FILING DATE: 2002-03-15
CURRENT FILING DATE: 2002-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/242,998 PRIOR FILING DATE: 2000-10-25 NUMBER OF SEQ ID NOS: 277
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                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 631
TYPE: DNA
ORGANISM: Homo sapien
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.94

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
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                                                                                                                                             563
                                                                                                                                                                                166
                                                                                                                                                                                                                   623
                                                                                                                                                                                                                                                    106
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                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                 CTTTGGAATAAAA 179
                                                                                                                                             CTTTAAATTAAAAA 550
                                                                                                                                                                                                                                                    GGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTT 165
                                                                                                                                                                                                                   GCAACTGAAGGGCTAACATTTATTGAGCCCCTTCTTTTTTGCCATGATCTTTGATATGTG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
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47; Conserv
                                                                                                                                                                                                                                                                                                         Similarity
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Chen, Sei-Yu
                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 4
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APPLICANT:

Algate, Paul A.

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US-09-745-763-204
; Sequence 204, Application US/09745763
; Patent NO. US20020065394A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-796-692-4354
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PRIOR FILING DATE: 2000-03-17
PRIOR PELICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/186,126 PRIOR FILING DATE: 2000-03-01
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CURRENT FILING DATE: 2001-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 TTTACATATATGCAGGGAAGTAATGGTACTGGTAGTGTATGTTTTCTATGTGGTTCAA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 TAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 ATGCTGCGTTGTTCAGCAGCCCCTCTGTGTTGTGTGATTTGTTTTATTTTTCCTTTTT 336
                                                                                                                                                                                                                                                                                                                                               215 GTCACAACCAAATTGAT 199
                                                                                                                                                                                                                                                                                                                                                                        294 GGCGCAGCTATGTTGGT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAATCAGGT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 AGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
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FILING DATE: 2000-07-14
APPLICATION NUMBER: 60/222,903
FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/223,378
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FILING DATE: 2000-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93;
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Similarity 47.28;
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            Treacy, Maurice
Spaulding, Vikki
INVENTION: SECRETED PROTEINS AND
                                                                                                 McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa P
Evans, Cheryl
                                                                                                                                                                                  Jacobs, Kenneth
                                                                          Merberg, David
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  ENCODING
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Pred. No. 3.9;
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THEM
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                POLYNUCLEOTIDES
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      SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2678
LENGTH: 26591
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-2678
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                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: Nuc FILE REFERENCE: PC005
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CORRESPONDENCE ADDRESS:
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Sequence 2678, Application US/09764877 Patent No. US20020147140A1 GENERAL INFORMATION:
                                               CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - NUMBER OF SEQ ID NOS: 4031
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SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 204:
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REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8384
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGACCTTTGGCACACTTGAAGGGATGGTGATGGAGATGCCAATCCATGGAATCAGGT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
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ilarity 47.2%;
Conservative
                                                                                                                     Nucleic Acids, Proteins,
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Pred. No. 1:
                           refer to PALM
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                    file wrapper
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; Sequence 1518, Application US/09764847
; Patent No. US20020132767A1
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US-09-822-849A-246
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Best Local S
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SEQ ID NO 246
LENGTH: 2648
                                                                                      GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1518
LENGTH: 1655
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CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                148 GTTGTTTAATCTAATGTTCTTTGGAATAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 207
                                                                                                                                                                                                                                                                                                                                          208 TGCTCAACATGCTTTG
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Local Similarity 51.5%;
hes 70; Conservative
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Agostino, Michael J.
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58.1%;
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Pred. No. 10;
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Pred. No. 24;
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US-09-818-512-3/c
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                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                     Sequence 3, Application US/09818512
Patent No. US20020142416A1
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Best Local Similarity
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APPLICANT: BEASLEY, Ellen et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN I
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL0011192
CURRENT FILLING DATE: 2001-03-28
UMBBER OF SEQ ID NOS: 4
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APPLICANT: Johannsdottir, Vala Drofn
TITLE OF INVENTION: Human Osteoporosis Gene
FILE REFERENCE: 2345.2009-001
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PRIOR FILING DATE: 2000-09-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapien FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (3639)...(3984)
NAME/KEY: CDS
LOCATION: (11757)...(1260)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1161 TGTTTTCCTTTGTTTTCCCTAAATTTCCTTTGAAGAACATGTCACCTGTC 1112
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                                                                                                                                                                                                                                                                                   8059 TIGITITGTTTCTTGTTTTTGTGACACAGGGTCTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                     8179 AATGAAACAGTTGCAGTTCAGAGAGGTTATGTAACTTTCCTAAGGTCACAGAGCTAGCAA 8120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 TCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCC 189
                                                                                                                                                                                                                                                                                                                        149 TTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 CTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGT 139
                                                                                                                                                                                                                                                                                                                                                                                              89 GCTTGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 AATGACGCAGCGGCTCTTAGAGGAACATATGGAAAACACCCAAGCCGGAGTCTCTCACAA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 49.4 nes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                             ATTAAAAGTAGATATATAATTGAATCTACTGCGCTTCTCAGGTTTCTTGTCTTTTGTT 8060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14759
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Pred. No.
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SOFTWARE: FastSEQ

for Windows Version 4.0

ID NO 3

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: LCCATION: (1)...(116592)
; OTHER INFORMATION: n - A,T,C
US-09-818-512-3
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                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (177)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (276)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (333)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (334)
NAME/KEY: misc feature
LOCATION: (334)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 12445
LENGTH: 438
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/420,856 PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dillon, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20063 ACTGATACTGGAAATACTATTCACAGGTGAGAAAACTT 20026
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             LOCATION: (345)
OTHER INFORMATION: n equals a,t,g, or
                                                                                    NAME/KEY: misc feature
LOCATION: (335)
OTHER INFORMATION: n equals
                                                               NAME/KEY: misc feature
                                                                                                                                                      OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 7.9%;
Local Similarity 49.4%;
les 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTAACTAATAAATGGTCTGTGGATAGGAAAGACCCCAAAGTAGCATAGCACAGTCTTTGA 20064
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misc feature
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Li, Haodong
                                                                                      a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB
Pred. No. 70;
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; LOCATION: (422)
OTHER INFORMATION: n equals a,t,9, or NAME/KEY: misc feature
; LOCATION: (429)
; OTHER INFORMATION: n equals a,t,9, or US-09-783-590-12445
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Search completed: January 31, 2003, 01:17:11 Job time: 157 secs
                                                                                                                                                                                                                               Query Match 7.8%;
Best Local Similarity 61.0%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (407)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (404)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature LOCATION: (395)
                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                   150 GAATGTGTTCTGCAGCTGATGGATGNAATGTTTTGTAAATGTCTGTTAGATCCATTTA 209
                                                                                                                                                                       93 GAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGT 152
                                                                                                              TTAATCTAATGTTCTTT 169
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Pred. No. 8.1;
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GenCore version 5.1.3 Compugen Ltd
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 23:50:38; Search time 52 Seconds (without alignments) 2229.304 Million cell updates/sec

Title: Perfect score: US-09-803-719-222 378 1 tacggctgcttaagacgact.....taccattggagaaccatgcg 378

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_NA: \*

Database

/cgn2\_6/ptcdata/1/ina/5A\_COMB.seq:\*
/cgn2\_6/ptcdata/1/ina/5B\_COMB.seq:\*
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/cgn2\_6/ptcdata/1/ina/6B\_COMB.seq:\*
/cgn2\_6/ptcdata/1/ina/BCTUS\_COMB.seq:\*
/cgn2\_6/ptcdata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	c 26	25	C 24						c 18		16	15	14	13	12	11	10				0		4	w	N	1	1 1 1	Result
28.8	28.8	29	29.2	29.2	29.2	29.2	29.2	29.2	29.2	29.2	29.4	29.4	29.4	29.4	29.4	29.4	29.6	•	29.6	•	30	30.4	31.6	31.6	31.6	31.6		Score
7.6	7.6	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.8	7.8	7.8	7.8	7.8	7.8	7.8	•			7.9		8.4	8.4	8.4	8.4		Query
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US-08-504-718D-14	US-08-504-718D-13	US-09-345-882-1	PCT-US95-02520-2	US-08-796-364-2	US-08-660-754-2	US-08-204-675-2	0	US-08-796-364-3	US-08-660-754-3	US-08-204-675-3	5217870-1	US-08-482-073-1	-490A-	US-08-344-155C-98	-08-365-470-1	0	-687-289A-	US-09-573-986-1	ò	US-09-134-618-3	-08-378-548-2	-593-995-1	-09-528-784A-	-08-723-142A-	US-08-990-571-10	US-08-845-258-10	• • • • • • • • • • • • • • • • • • •	TD.
14,	e 13,		N	N	N,	Sequence 2, Appli	ω	ω '	'n	Ge Co	Patent No. 5217870	_	88,	, 86	ш	18		<b>,</b>	۳,		24,	10,	10,		10,	Sequence 10, Appl		70000111100

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27.6	27.6	27.6	27.6	27.6	28	28	28	28	28	28	28	28.2	28.4	28.4	28.8	28.8	20.0
7.3	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.5	7.5	7.5	7.6	7.6	
4389	3195	3195	2298	2298	11478	11478	699	376	376	376	. 376	1068	2358	2259	1205	420	27.5
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US-08-951-648-3	US-09-174-437-5	US-08-951-648-5	US-09-174-437-1	US-08-951-648-1	US-08-983-440-29	US-08-981-803-29	US-09-221-017B-169	US-08-983-440-23	US-08-983-440-9	US-08-981-803-23	US-08-981-803-9	US-08-427-640-7	US-09-134-001C-1029	US-07-828-700-7	US-09-017-754A-19	US-08-504-718D-16	02-00-304-1T0D-T3
Sequence 3, ,	Sequence 5, 1	Sequence 5, A	Sequence 1, A	Sequence 1, Appl	Sequence 29, Appl	Sequence 29, Appl	Sequence 169,	Sequence 23, Appl	Sequence 9, Appl	Sequence 23, Appl	Sequence 9, Appl	Sequence 7, Appl	Sequence 1029, Ap	Sequence 7, Ap	Sequence 19, Appl	Sequence 16, 1	sequence is,

## ALIGNMENTS

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US-08-845-258-10
                                                                                                                                                                         CURRENT APPLICATION.

APPLICATION NUMBER: US/08/843,222
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1050-6031
TELEFAX: (206) 662-4900
TELEFAX: (206) 662-6031
TELEFAX: 870 SEQ ID NO: 10:
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                                                                                                                TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDENNESS: single
Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08845258
Patent No. 6183976
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                       ZIP: 95104
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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  8.4%;
ilarity 51.4%;
Conservative
                                                                                               linear
Score 31.6; DB Pred. No. 1.6; 0; Mismatches
    0;
                                    DB 4;
    69;
                                        Length 3701;
    Indels
  0
Gaps
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RESULT 3
US-08-723-142A-10
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51...
Conservative
                                                     Sequence 10, Application US/08723142A Patent No. 6306396
                       GENERAL INFORMATION: APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08990571 Patent No. 6214971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION UNMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
           APPLICANT:
                                                                                                                                                                                                         1059 TTTATATAATCATATATATTATATAATTATATATATATTTGATAATTGAATATATCAATAAT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 11-DEC-19
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1059
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                                                                                                                                                                                262 GGTGATGGAGATGCCAATCCAT 283
                                                                                                                                                                                                                                        202 GTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT 261
                                                                                                                                                                                                                                                                       999 TATTCTACTTTTTAATATATTTTTTTTTTCAATAATATACTCTTTCATATTTTGTACTAT 1058
                                                                                                                                                                                                                                                                                           142 TTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAACCTCCCTGCCAAGTAGTACTTG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
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                                                                                                                                                    GATGATATACATGAATATGCAT 1140
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VENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF
      Reed, Steven G
Lodes, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-09-528-784A-10
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US-08-723-142A-10
                          SOFTWARE: F
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APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.425C4
                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                       CURRENT APPLICATION NUMBER: US/09/528,784A CURRENT FILING DATE: 2000-03-17 NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                        APPLICANT:
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 0: CLASSIFICATION:
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No. 6451315
                                           FastSEQ
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                                                                                                                                                                                                      Lodes, Michael J
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TELEFAX: (206)682-603: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOPPY PC - DOS/MS - DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
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APPLICATION NUMBER: US/08/723,142A
FILLING DATE: 01-OCT-1996
                                                                                                                                                   999 TATTCTACTTTTAATATATTTTTTATTCAATAATATACTCTTTCATATTTTGTACTAT 1058
                                                                                                                                                                           142 TTTTCCGTTGTTTAATCTTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTG 201
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                                      262 GGTGATGGAGATGCCAATCCAT 283
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                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                          GTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT 261
GATGATATACATGAATATGCAT 1140
                                                                       TTTATATAATCATATATATATATAATTATATATATTTGATAATTGAATATATCAATAAT 1118
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Pred. No. 1.
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                                                                                                                                                                                                                                                  Sequence 24, Application US/08378548 Patent No. 5981177
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CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/139,121
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20598
                                                                                                                                                                   APPLICANT: Demirjian,
APPLICANT: Casadaban,
APPLICANT: Weber, J. N
APPLICANT: Gaines III.
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                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                   TITLE OF INVENTION: Protein Fusion Method and Constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 TIGITIAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTAT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 TTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAACCTCCCTGCCAAGTAGTACTTG 201
COMPUTER READABLE FORM:
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mes 64; Conserv
                                                CITY: Chicago
STATE: Illino:
                                                                               STREET:
                             COUNTRY:
                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                       TTTCAATTTCATTTTACCATCAAGAAAAGAGCGTTAAGCAAAATAAAACTCATTCTGATG 17306
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                                                                                                                                                                                                                                    INFORMATION:
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                   60606
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                                                Illinois
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                                                                              E: Banner & Allegretti, Ltd.
Ten South Wacker Drive
                                                                                                                                                               Weber, J. Mark
Gaines III, George L.
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Pred. No. 1.6;
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US-09-134-618-3/c
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Best Local Similarity
Matches 54; Conserv
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                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09134618 Patent No. 6417328
                                                                                                                        Matches
                                                                                                                                                        Query Match
                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 480140.432
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/134,618 CURRENT FILING DATE: 1998-08-14
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 6
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                              NAME/KEY: CDS
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REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 7003 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Chao, Mark
                                                                                120 CACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 AAAACCTCCCTGCCAAGTAGTACTTGGTTTTATG 209
              180 CCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGAC 239
                                                 429 CATGGTGCAGGAACTTTTATGTTTTTGATCTGATTTACAAACTGTACATGGGAAGCAAGA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 GATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 1..7003
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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)EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7003 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312-715-1234
                                                                                                                        Conservative
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48.3%;
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                                                                                                                                        Score 29.6; Di
Pred. No. 3.7;
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                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEIC ACIDS ENCODING SAME,
                                                                                                                                                        DB 4; Length 900;
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Best Local Similarity
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Re-
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                 FEATURE:
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                         240
                                                       431 AGGTTCATTGTTGGAAGCGTTGGTGTAATCCACACCCTCTGTGCACGGGTTACAGGCTCC
                                                                                              180
                                                                                                                        491 CATGGTGCAGGAACTTTTATGTTTTTGATCTGATTTACAAACTGTACATGGGAAGCAAGA 432
                                                                                                                                                       120 CACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAA 179
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/006,353A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
     CTTTGGCACACTTGAAGGGATGGTGATGGAGATGCCAATCCATGGAATCAG
                                                                                         CCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAAGAGAC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGTTCATTGTTGGAAGCGTTGGTGTAATCCACACCCTCTGTGCACGGGTTACAGGCTCC 310
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YU, GUO-LIANG
GENTZ, REINER
RUBEN, STEVEN
                                                                                                                                                                                          7.8%;
ilarity 48.3%;
Conservative
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183..959
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261..959
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183..260
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Pred. No. 4.6;
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                                                                                                                                                                                                                         DB 4;
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; LOCATION: (18:
US-09-573-986-1
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US-09-573-986-1/c
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Best Local Similarity
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SEQ ID NO 1
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APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Nev
FILE REFERENCE: 1488.1280004
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CURRENT APPLICATION NUMBER: US/09/573,986
CURRENT FILING DATE: 2000-05-18
                                                                                                                                                                                                                                                   APPLICANT: Hammerlan
TITLE OF INVENTION:
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 CCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGAC 239
                                                                                                                                      CITY: Los Angeles
STATE: California
                                                                                                                                                                   ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 AGTATGTTCTGATCTATGAGATCCTGCTGGACACTCCTCCCCCTTGAAGCTG 320
                                                  MEDIUM TYPE:
                                                                                                         COUNTRY: U.S.A. ZIP: 90071-2066
                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTATGTTCTGATCTATGAGATCCTGCTGGACACTCCTCCCCCTTGAAGCTG 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08687289A
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                                                                                                                                                                                                                                                                                                                                Hammerland, Lance G.
VENTION: CHIMERIC RECEPTORS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                      Fuller, Forrest H.
SYSTEM: IBM P.C. DOS 5.0 FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                        Krapcho, Karen J.
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                               IBM Compatible
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Pred. No. 4.6;
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Length 1392; Indels

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                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Monia, Brett P.
APPLICANT: X1aoXing S.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-0336
                                                                                                                                                           NAME/KEY: CDS
LOCATION: (117)..(1949)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: M24736/Genbank
DATABASE ENTRY DATE: 1994-11-07
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/209,668A CURRENT FILING DATE: 1998-12-10 NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 220,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                             LENGTH: 3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 4000 base pairs
 3192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1738 GGAGTGTCCTGATGGGGAGTATAGTGATGAGAGAGATGCCAGTGCCTGTAACAAGTGCCC 1797
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                 114 AGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 7.8%;
Local Similarity 50.7%;
nes 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/
FILING DATE: July 25, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                     Local Similarity
AAGATGTCTAATAGTTATTCCCTATTTGTTTTCTTCTGTATGTTAGGGTGCTCTGGAAGA 3251
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Pred. No. 7
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                                                                                     Score 29.4;
Pred. No. 8
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US-08-365-470-1
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                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/850
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
AMBE: MARKOWICZ, Karen R.
REGISTRATION UNMBER: 36,351
REFERENCE/DOCKET NUMBER: 0627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                  3192 AGGATGTCTAATAGTTATTCCCTATTTTGTTTTCTTCTGTATGTTAGGGTGCTCTGGAAGA 3251
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APPLICATION NUMBER: US 08
FILING DATE: 05-AUG-1993
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MEDIUM TYPE: Floppy
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                                                                  3252 GAGGAATGCCTGTGTGAGCAAGCATTTATGTTTATTATAAGCAGATTTAACAATTCCAA 3311
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                   114 AGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: herewi
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AGGAATCTCCAGTTTCAGTTGATCACTGGCAATGAAAA 3350
                          AGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGA 272
                                                                                                TAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAA 233
                                                                                                                                                                                                                                                                                                                    nucleic acid
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nilarity 49.1%;
Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/365,470
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Pred. No. 8.6;
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                                                                                                                                                                                         Matches
                                                                                                                                                                                                                         Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (609) 779-8488 INFORMATION FOR SEQ ID NO:
                                                3276 GAGGAATGCCTGTGTGAGCAAGCATTTATGTTTATTATAAGCAGATTTAACAATTCCAA 3335
                                                                                                                    3216 AAGATGTCTAATAGTTATTCCCTATTTGTTTTCTTCTGTATGTTAGGGTGCTCTGGAAGA 3275
                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
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APPLICATION DATA:

FILING PART
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PRIOR APPLICATION NUMBER: 07/567,286
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PRIOR APPLICATION DATA:
08/007,997
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TITLE OF INVENTION: Compositions and Methods for Preventing
TITLE OF INVENTION: and Treating Allograft Rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: September 2, 1992
PRIOR APPLICATION DATA:
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234 AGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGA 272
                                                                                        174
                                                                                                                                                     114 AGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
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                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                       TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 9/2/92
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les 78; Conserv
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                                                                                     TAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAA 233
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                                                                                                                                                                                                                                                                                                                                               3858
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210 Lake Drive East, Suite 201
                                                                                                                                                                                      7.8%;
ilarity 49.1%;
Conservative
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5883082ember 23,
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                                                                                                                                                                                    Score 29.4; DB Pred. No. 8.6; 0; Mismatches
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US-09-009-490A-88
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GENERAL INFORMATION:
                                                                                                                                     Matches
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO
3276 GAGGAATGCCTGTGTGAGCAAGCATTTATGTTTATTATAAGCAGATTTAACAATTCCAA 3335
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: August 14, ATTORNEY/AGENT INFORMATION: NAME: Jane Massey Licata
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APPLICATION NUMBER
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                                                                    3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: January 20, 1993 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT (CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                       174
                                                                                      114 AGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAA 173
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                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 063,167 FILING DATE: May 17, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: J. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: February 10, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                  Local Similarity 49.1
es 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/009,490A
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                                                             AAGATGTCTAATAGTTATTCCCTATTTGTTTTCTTCTGTATGTTAGGGTGCTCTGGAAGA 3275
                              TAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGTTGAAA 233
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VENTION: Oligonucleotide Modulation
VENTION: of Cell Adhesion
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May 12, 1995
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49.1%;
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234 AGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGA 272

AGGAATCTCCAGTTTTCAGTTGATCACTGGCAATGAAAA 3374

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RESULT 15
US-08-482-073-1
                                    Query Match
Best Local S
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APPLICATION NUMBER: WO PCT/US 90/02357

FILING DATE: 27-APR-1990

PRIOR APPLICATION NUMBER: US 07/452675

FILING DATE: 18-DEC-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/359516

FILING DATE: 01-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION DATA:
                   Matches
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                                                                                                                                                                                                                  TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/354151
FILING DATE: 28-APR-1989
ATTORNEY_AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B124CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3863 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,073
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,336
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ZIP: 10020
COMPUTER READABLE FORM:
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TITLE OF INVENTION:
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7.8%;
Local Similarity 49.1%;
tes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
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1251 Avenue of the Americas
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Benjamin, Christopher D.
Rosa, Margaret D.
VENTION: ENDOTHELIAL CELL-LEUKOCYTE ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hession, Catherine A.
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            Score 29.4; D
Pred. No. 8.6;
0; Mismatches
                                                 DB 4; Length 3863;
            81;
            Indels
            0:
          Gaps
          0;
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Search completed: January 31, 2003, 01:14:56 Job time: 88 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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378
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AI459918 ar81h09.x
AA743908 ob05510.s
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AQ035618 CIT-HSP-2
AQ035738 CIT-HSP-2
                                                                                               Description
                                                                  BM987874 UI-H-COO
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AUTHORS
TITLE
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VERSION
KEYWORDS
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BM987874/c
LOCUS
              FEATURES
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ORGANISM
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                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov
                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 451)
NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Onpublished (1997)
                                                                                                                                                                                                                                                                                                               UI-H-COO-asz-a-11-0-UI.sl NCI_CGAP_Sub9 Homo sapiens cDNA clone IMAGE:5860149 3', mRNA sequence.
                         Seq primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                                                                                                      human.
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Location/Qualifiers
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AI781854
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AQ775948
AI350894
AI600177
AW704405
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AL628007
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BJ068145
AZ534719
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AW190856
AZ083843
AW444676
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AW231608
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AZ400532
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A2182814
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BM973205
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AZ108808
AZ191123
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вн853295
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A1651773 wb50b04.x AA711119 vt56b05.x AW635726 b137d10.w BJ068145 BJ068145 AZ534719 ENTBW93TR

EST 17-JUN-2002

AQ419832 RPCI-11-1 AW190856 x142£09.x AZ083843 RPCI-23-2 AW444676 UI-H-BBI3-BQ024523 UI-1-BBIP AZ182824 SP\_0190\_A

SP\_0190\_A MR4-BT035

AI781854 EST262733 AZ720218 RPCI - 24-1 BM973205 UI - CF - EC1 BB566524 BB566524 AZ122814 SP - 0190\_A BIB61604 603390466 AV413421 AV413421

AW704405 sk30f07.y AL055267 Drosophil

AZ400532 1M0166D23 AL274426 Tetraodon AW231608 687067H09 BB481722 BB481722 AI828325 wk83d06.x

AQ922388 RPCI-23-2 AZ108808 RPCI-23-2 AZ191123 SP\_1018\_B AI449346 mt07d11.x AQ775948 HS\_2151\_B AI350894 gt13d12.x AI600177 EST251880

BQ392762 NISC\_mq26 AL628007 AL628007

BQ655384 NXRV093\_F BH853295 SALK\_0763 BI454874 603173414

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REFERENCE
AUTHORS
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ORGANISM
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AI459918/c
                                                                                                                                   COMMENT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 ATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGCAGAAGTC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCTTGGCAAAGATTCCTCCCGGGAAGGAAGGTACCATTGGAGAACCATGC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGAGATGCCAATCCATGGAATCAGGTGGCACAGCTATGTTGGTAGCTATAGCAGAAGTC
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 43)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project
                     Washington University School of Medicine 4444 Forest park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                             Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI459918
AI459918.1 GI:4312799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI459918 439 bp ar81h09.xl Barstead colon HPLRB7
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE: 2151713 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinoma, Bladder carcinoma, Brain oligodenroga;
NCI_CGAP_Sub9 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are CGTC, AACG, GGGCC, GGAAG, TAGC, TAAGC, ATGG, AGCA, ATCAC. For additional differentiation.
est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (Life Technologies)"
/note="Vector: p7773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; tissues: Cholonic mucosa with Crohns disease, Cholonic mucosa with ulcerative colitis, Fetal thymus, Cervix, Cervical adenosquamous carcinoma, Ligament cells, Prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_TISSUE-Prostate Carcinoma
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/clone_lib="NCI_CGAP_Sub9"
/tissue_type="mixed"
/dev_stage="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           information, contact: Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%;
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                                                                          St. Louis,
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KEYWORDS
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AA743908/c
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                                                                                                                                                                                                          TITLE
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Best Local Similarity
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                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120;
                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Insert Length: 508 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 234.
Location/Qualiflers
                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 386)
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                  AA743908.1 GI:2784658
                                                                                                                                                                                                                                                                                                                               mRNA sequence.
AA743908
                                                                                                                                                                                                                                                                                                                                                      AA743908 386 bp mRNA linear EST 19-FEB-199
ob05b10.sl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322779 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Gibco
                                                                                                                                                                                                    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 425.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:1322779"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barstead."
                                                                       1. .386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2151713"
                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Barstead colon HPLRB7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ب</u>
                                                                                                                                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 439;
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                                                                                                                                                                                                                                                           Euteleostomi;
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/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

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REFERENCE
AUTHORS
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DEFINITION
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BG197212/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
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                                                                                                            Query Match
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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262 GGTGATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGCAG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 CTTCTTGGCAAAGATTCCTCCCGGGAAGGAAGGTACCATTGGAGAACCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 ATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTAGGTAGCTATAGCAGAAGT 325
                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotte; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 806)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Velso,N., Kiika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                               Email: scain@athersys.com
High quality sequence stop: 417.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG197212 806 bp mRNA linear EST 21-APR-2001 RST16451 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
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                                                                                        Similarity
                                                                                                                                                                          252
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                                                                                                                                                               /note="See 'Creation of Genome-wide Protein Expression', Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

187 c 155 g 205 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector: mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                       /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                         . 806
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77 c 73 g
                                                                                    21.0%;
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                                                              Score 79.4; Di
Pred. No. 2.6e
0; Mismatches
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Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
                                                                             AQ035738
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Unpublished (1998)
Other_GSSs: CIT-HSP-2319N3.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of a random BAC End Sequence Database for Sequence-Ready Map
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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349 bp DNA linear GSS 11-JUL-1998
CIT-HSP-2319N3.TF CIT-HSP Homo sapiens genomic clone 2319N3, DNA
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                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Sperm"
/note="Yector: pBeloBAC11; Site_1:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="2319N3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CIT-HSP"
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Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                            Sederoff, R.
                                                                                                                                                                                                                                                                       Pinus taeda
                                                                                                                                                                                                                                                                                                                                         B0655384 p mXRV093_F11_F NXRV (Nsf Xylem Root w clone NXRV093_F11 5', mRNA sequence.
                                                                                               Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                                                                                                    BQ655384
BQ655384.1 GI:21787710
                                                                                                                                                                                         Molecular Basis of Wood Formation
                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_GSSs: CIT-HSP-2321C21.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
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Seq primer: M13-21
Class: BAC ends.
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Clones are available from Research
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9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Homo sapiens
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                                                                                   primer: T3
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/organism="pinus taeda"
/strain="Coastal plain loblolly pine
/db_xref="taxon:3352"
                                                                 Location/Qualifiers
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/clone_lib="CIT-HSP"
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/db_xref="taxon:9606"
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/note="Yector: pBeloBAC11; Site_1: HindIII;
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C., Shizuya,H.,
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             North Carolina"
                                                                                                                                                                                                                                  Tracheophyta;
Pinus; Pinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTG 227
                                                                                                                                                                                                                                                                                  Arabidopsis Genome
(7001)
(Onpublished (2001)
(Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
(10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                  This is single pass sequence recovered from the left border TDNA. This sequence lies within 300 bases of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (Dases 1 to 439)
1 (Dases 1 to 439)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab
Alonso, J.M., Kerse, M., Kim, C.J., Parker, H., Prednis, L., Shinn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH853295 439 bp DNA linear GSS SALK_076311.54.00.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK_076311.54.00.x,
                                                                                                                                                                                    Class: TDNA tagged.
                                                                                                                                                                                                           At2g41810
                                                                                                                                                                                                                                                                 Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                        ,C., Jeske,A., Karnes,M., Kim,Č.J., Parker,H., Prednis,L
, Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH853295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thale cress.
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/db_xref="taxon:3702"
/clone="SALK_076311.54.00.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
                                                                                              /strain="Columbia
                                                                                                                   /organism="Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="XL1-Blue"
//note="Vector: pBlueScript SR-; Site_1: Eco RI; Site_2:
XhoI; The library is from primary xylem scraped from the
roots of a twelve year old tree in the transitional phase
from juvenile wood to mature wood production. NOTE: The
sequences contain a 'cDNA adapter' between the EcoRI site
and the start of the EST. The adaptersequence is
'AATTCGGCACGAG'."

88 c 131 g 161 t 21 others
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="NXRV093_F11"
/clone_lib="NXRV (Nsf xylem Root wood Vertical)"
/tissue_type="xylem"
/cell_type="Root (primary)"
/dev_stage="Transitional"
                                                                                                                                             . 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:21424166
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                                                                                                                   thaliana'
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KEYWORDS
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BI454874/c
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JOURNAL
                  Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 GGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243
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                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nlh gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                             Plate: LLAM11638 row: 1 column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999 Contact: Robert S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                  Similarity
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                                                                                           431
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                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 102
Location/Qualifiers
1 1237
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                                                                                                                     /note-*Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall
Site_2: NotI; Cloned unidirectionally. Primer: Oligo do
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html* 68 c 68 g 146 t 2 others
                                                                                                                                                                                             /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:5252883"
                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Mam5"
                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
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                  10.3%;
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                  Score 38.8;
Pred. No. 1.
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 93;
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Indels
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A clone
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IMAGE:5252883 5',
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BQ392762
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                                                                            144 TTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTACTACTTGGT 203
204 TTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACACTTGAAGGGATGG
                                                     405 TTGCCATGGAGACTCTGATTTCCTTGGGATTTGAAAGGGTTCTTACTAGTGGCTGTGACA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
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                                                                                                                                  l Similarity
83; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                           info@image.llnl.gov
Plate: LLAM11980 row: G column:
Seq primer: M13RP1 reverse primer
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
cDNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.

[ bases 1 to 585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
National Institute of Child Health and Human Development, National
Cancer Institte, Xenopus Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            western clawed frog.
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                                                                                                                                Conservative
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                                                                                                                                                                                                                 /clone_lib="NICHD XGC Emb5"

/tissue_type="gastrula"
/dev_stage="embryo, stages 10-13"
/lab_host="DH10B (phage-resistant)"
/note="Vector: pCMV-SPORT6.ccdb; Site_1: Not1; Site_2 EcoRY; Cloned unidirectionally, Primer: Oligo dT. Ave insert size 2.0 kb. Constructed by Invitrogen. Note: is a Xenopus Gene Collection (XGC) library."

109 c 163 g 172 t
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Silurana tropicalis"
/db_xref="taxon:8364"
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                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5384863"
                                                                                                                                                  10.1%;
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                                                                                                                                                  Score 38; DB 14; Pred. No. 2.6;
                                                                                                                              Mismatches
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Euteleostomi;

de Jong, P

Akinret

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RESULT 12
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Best Local (
                                                                                                                                                                                                                                                               204 TTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTTGGCACACATTGAAGGGATGG 263
                                                                                                                                                                                                                                                                                                                                                144 TTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAACCTCCCTGCCAAGTAGTACTTGGT 203
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                                                                                                                                                                            TCATAGTAATGCCAGGTGGCGGCATTACTGAGCGAAAC 606
                                                                                                                                                                                                                                           CGTCTGCTTTGGAAGGTTTGCCTTTAATAAAGAGACTTGTGGAACAAGCCAAAGGACGAA 568
                                                                                                                                                                                                                                                                                                               TTGCCATGGAGACTCTGATTTCCTTGGGATTTGAAAGGGTTCTTACTAGTGGCTGTGACA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATGGAGATGCCATCCATGGAATCAGGTGGCGCAGC 301
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                                                                    RPCI-23-27685.TJ RPCI-23
                AQ922388
AQ922388.1 GI:6611391
                                                   DNA sequence.
                                                                                            AQ922388
                                                                                                                                                                                                                                                                                                                                                                                                 83;
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas022e21.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huckle,E., Taylor,Ř., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001) Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Silurana tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="TGas022e21"
/clone=lib="XGC-gastrula"
/cloue_lib="XGC-gastrula (stages 10.5-13 mixed)"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli xL1-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI out cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Silurana tropicalis"
/db_xref="taxon:8364"
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                                                         Mus musculus genomic clone RPCI-23-276B5,
                                                                                     592 bp
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                                                                                                                                                                                                                                                                                                                                                                              109 GCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTTGTTTAATCTAATGTTCTT 168
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                                                                                                                                                                                                                                       TGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAAT
                                                                                                                                                                                                                                                                            TGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGT 228
                                                                                                                                                                                                                                                                                                                                               DNA sequence.
AZ108808
                         RPCI-23-25N18.TV RPCI-23
                                                     AZ108808
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Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
seg primer: 276 row: B column: 5
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                  580
                                                                                                                                                                                   291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Sha, Levins, M., Mcgann, S., Tsegaye, G., Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; i
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 592)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="RPCI-23-276B5"
/clone_lib="RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
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Pred. No. 3.9;
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                    Mus musculus genomic clone
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288 517

GSS 09-MAY-2000 RPCI-23-25N18,

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REFERENCE
AUTHORS
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AZ191123

B29 bp DNA linear GSS 30-AUG-2000 SP_1018_B2_D06_T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1018 Col-12 Row-H, DNA sequence.

AZ191123

AZ191123.1 GI:8374302
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Other_GSSs: RPCI-23-25N18.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tlgr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BACPAC Resources (http://bacpac.med.buffalo.edu) buffalo.edu/orderingframe.htm)
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 25 row: N column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T7
Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 699)
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/clone="RPCI-23-25N18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                      521 GCTAGCCAACGCTG 508
                                                                                                                                                                                                                                                                                                                                                                                                                          271 GATGCCAATCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 TCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGATGGA 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
Mus musculus

Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 4/3)

1 (bases 1 to 4/3)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Cameron, RA, Davidson, EH
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                              AI449346
mt07d11.x1 Soares mouse
3', mRNA sequence.
AI449346
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Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 1018 row: H column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  additional resources
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                                                                                                                                                                                                               AI449346.1
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Class: BAC ends
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Location/Qualifiers
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/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
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DH108"
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/db_xref="taxon:7668"
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Pred. No. 5.5;
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musculus
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Best Local Similarity 54.4%;
Matches 74; Conservative
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JOURNAL
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                                                              241 TTTGGCACACTTGAA 256
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168 TTGGGCCTACATTGAA 183
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                                                                                                                                                  181 CTCCCTGCCAAGTAGTACTTGGTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACC 240
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                                                                                                                                                                                              CTCACAGTAAACCTTTTGTGGTTTTAATGACTTGCATATGTTGCCAATTAAAAGGATTCA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 402.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra W.MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                         143 a
                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:620373"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="Soares mouse 3NbMS"
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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              378
299.6
279.6
33.8
33.6
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33.4
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SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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Copyright (c) 1993 - 2003 Compugen
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AAS37218
AAS37237
AAS37242
ABL337242
ABL33784
ABA08523
AAC29807
AAC24100
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(without alignments)
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## ALIGNMENTS

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XX O9-A
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PA (C Williams LT, Escobedo J, Innis MA, Gar Reinhard C, Randazzo F, Kennedy GC, Po Drmanac R, Crkvenjakov R, Dickson M, I Leshkowitz D, Kita D, Garcia V, Jones 09-MAR-2000; 2000US-0188609 Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC. 09-MAR-2001; 2001WO-US07787. 13-SEP-2001. WO200166753-A2. Homo sapiens 17-DEC-2001 AAS37164; Novel human diagnostic and therapeutic gene #222 AAS37164 standard; cDNA; 378 (first entry) ВP Garcia PD, Sudduth-Klinger
Pot D, Kassam A, Lamson G
, Drmanac S, Labat I;
nes WL, Stache-Crain B;

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WPI; 2001-530177/58

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                      09-MAR-2000;
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378; Conserv
                                                                                                                                                                     human diagnostic and therapeutic gene #276
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CHIRON CORE
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ative 0;
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                                                                                                                                             colon; prostate; cytostatic; diagnostic;
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Pred. No. 2.8e-112;
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RESULT 3
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Reinhard C,
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Leshkowitz D,
                                                                                                       Novel
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Crkvenjakov R, Dickson M, I
D, Kita D, Garcia V, Jones
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Stache-Crain B
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WO200166753-A2

for

diagnosis

ac S, Labat : Stache-Crain

Kassam A,

Sudduth-Klinger Labat I; 8 Lamson

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                                                                                                               Novel human diagnostic and therapeutic gene #300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 670; 1193pp; English.
                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US07787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INC
                                                                                        breast;
                                                                                                                                                                                                  CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.0%;
98.6%;
                                                                                      lung; colon; prostate; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garcia V, Jones WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 279.6;
Pred. No. 2e-8
0; Mismatches
                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcia PD, Sudduth-Klinger
Pot D, Kassam A, Lamson
, Drmanac S, Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ac S, Labat I;
Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sudduth-Klinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                               321
                                                                                                                                                                                                                                                                                       313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ი</u>
                                                                                                                                                                                                                                                                                                                                        267
                                                                                                                                                                                                                                                                                                                                                                                          207
                                                                                                                                                                                                                                                                                                                                                                 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
    RESULT 5
ABL33878
ID ABL3
XX ABL3
AC ABL3
XX DT 26-M
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
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XX Anti
KW anti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to new polynucleotides and polypeptides, useful fo diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39338 represent novel human diagnostic and therapeutic coding
                                                                                                                                                   ABL33878
                                                                                                                                                                         ABL33878 standard; DNA; 5378
                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 318 BP; 90 A; 63 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams LT, Escobedo J, Innis M
Reinhard C, Randazzo F, Kennedy (
Drmanac R, Crkvenjakov R, Dickso
Lashkowitz D, Kita D, Garcia V,
                                                                                                                                                                                                                                             276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 671; 1193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides and polypeptides, useful treatment of breast, lung and colon cancer -
                                                                                                                                                                                                                                                                     268
                                                                                                                                                                                                                                                                                               216
                                                                                                                                                                                                                                                                                                                                                 156
                                                                                                                                                                                                                                                                                                                          208
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-2000; 2000US-0188609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-2001; 2001WO-US07787
                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 GAATGACGCAGCGGCTCTTAGAGGAACATATGGAAAACACCCCAAGCCGGAGTCTCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                         GGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGT 310
                                                                                                                                                                                                                                                                                       TGCTCAACATGCTTTGACTGTTGAAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT
                                                                                                                                                                                                                                        GGAGATGCCAATCCATGGAATCAAGTGGCACAGCTATGTTGGT 318
                                                                                                                                                                                                                                                                                                     TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACACTTGAAGGGATGGTGAT 267
                                                                                                                                                                                                                                                                                                                                                                                              AGCTTGAATGTGTTCTTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                             AGCTTGAATGTGTGTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCTGTTCTTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATGACGCAGCAGCTCTGAGAGGAACATAAGGAAAAACACCCAAGCCGGAGTCTCTCACA
                                                                                             immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention.
                                                                                        associated gene SEQ
                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.8%;
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Kennedy GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                                                                                                                         ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 275; DB 22; Pred. No. 6.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones
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Pot D, Ka
, Drmanac S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
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5

Indels

0;

Gaps

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215 207 155 147 95 87 Length 318;

NO:

1851.

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RESULT 6
ABA08523
ID ABA0
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AC ABA0
XC ABA0
XX
DT 11-J
XX
Huma
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DE Huma
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Huma
KW Huma
KW 1nhi
KW proli
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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            inhibin; chemo
proliferation;
                 Human; cytokine; cell proliferation; cell differentiation; grammatopolesis regulation; tissue growth; immunomodulator; acinhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
                                                                        Human
                                                                                              11-JAN-2002
                                                                                                                                                                                                     1.557
                                                                                                                                                                                                                                                    1497
                                                                                                                                                                                                                                                                                                1437
                                                                                                                                                                                                                                                                                                                                                1377
                                                                                                                     ABA08523;
                                                                                                                                           ABA08523 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of human immune system associat genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, theumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising for diagnosis and treatm cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5378 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                          317
                                                                                                                                                                                                                                                                                                                       197
                                                                                                                                                                                                                                                                                                                                                                      137
                                                                                                                                                                                                                                                              GGGATGGTGATGGCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTAT
                                                                                                                                                                                                                                                                                                          ACTTGGTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCCTTTGGCACACATTGAA
                                                                                                                                                                                                                                                                                                                                                                 TGTTCTTTTCCGTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGT
                                                                                                                                                                                                    AATTGAGTAATTATTAG
                                                                                                                                                                                                                                                                                            ACGAAGTTTAGTGATTTATTTCGGATCGTTGTTGAGAATGGAGGTTTTTTAAATATTAAG
                                                                                                                                                                                                                                                                                                                                            AGCAGAAGTCTTCTTGG
                                                                        secreted
                                                                                                                                                                                                                                               2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                             95;
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a gene
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-EP07537
                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO 1851;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rising fragment of chemically modified treatment of diseases associated with
                                                                                                                                          CDNA; 492
                                                                                                                                                                                                                                                                                                                                                                                                      48.2%;
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                                                                    homologue-encoding
                                                                                                                                                                                                                          333
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; 134 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin
                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3.1.
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.8;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1201 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the
                                                                                                                                                                                                                                                                                                                                                                                                                                        2544 T;
                                                                     CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                           102;
                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                      0 other;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Length 5378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bowel disease;
                                                                     NO:299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene, useful
abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences
                                          growth
                               activin;
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                         factor;
                                                                                                                                                                                                                                                                                           1496
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                                                                                                                                                                                                                                                                                                                                                                  196
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CC haematopoiesis regulatory activity; tissue growth activity;

CC haematopoiesis regulatory activity or inhibin-related activities;

CC chemotactic or chemokinetic activities; haemastatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

cc involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC the invention are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC varcial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

cc immunomodulatory activities may be used in the treatment of viral,

CC polypeptides with growth factor activity may be used in cell cultures to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC manipulate disease or accidental damage. The polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug

CC constrains and in drugs the polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasctropic; cardiant; virucide; antibac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 440; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000;
27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US03800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human proteins and DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ofeins and DNA encoding sequences useful for preventing, or ameliorating a medical condition in a mammalian subject
                                                                  techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                        polypeptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0496914
2000US-0560875
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                                                                  The
                                                           present sequence represents
                                           the
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                                                                                    The present sequence is one of a large number of 5' ESTs derived from C mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA ilbraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer C cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and contromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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Query Match
Best Local Similarity
Matches 70; Conservat
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                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                              Sequence
                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 33882; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein 5' EST, SEQ ID NO: 33882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC29807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC29807 standard; cDNA; 158 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 TIGAATGTGTGTTCTGGAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGTTCTTTTCCGTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAACATGCTTTGACT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATATAATGTGCTGATTTTAACAATGCAGGCCTCACTGCCAAAAGTTCTTCGGGTTTTGTGC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAACCTCTACGCTCTTGGGTTGGGGTCATCAGATACCTGGGTTATTTCCAGGC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%;
Similarity 52.9%;
                                                                158
                                                              B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9905-0122487
                                                            35
                                                            A; 34 C; 34 G; 55 T; 0 other;
            53.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duclert A,
              Score 33.4;
Pred. No. 0.
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Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano
                0.9;
                            DB 21;
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                            Length
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Mismatches

61;

Indels

0,

Gaps

0

ΧĦ

AAZ24100 standard;

DNA;

240

RESULT 9 AAZ24100/c

밁 QY

60

148 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTT 206

N

Matches Query Match Best Local :

Local Similarity

8.8%; 72.9%;

Score 33.4; DI Pred. No. 1.1; Mismatches

DB 20; 16;

Length Indels

0

0

Conservative

0;

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RESULT 8
AAZ24099/c
ID AAZ240
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                        This invention describes a novel method for determining the absolute mutagenicity of a substance. The method is used to determine the mutation rate associated with particular substances and the error rates for polymerases during amplification reactions. It is therefore useful for monitoring nutrients or medicines and environmental factors such as radiation from televisions or computer screens. The method is applicable to all types of mutations (collectively or individually), is unaffected by repair mechanisms or in vivo selection mechanisms, and is an in vitro process so animal testing is not required. AAZ24098-Z24105 represent rat NF-1 DNA fragments used to illustrate the method of the invention.
Sequence 240 BP; 66 A; 53 C; 53 G; 68 T; 0 other;
                                                                                                                                                                                                                              Method for determining absolute mutagenicity and error rate polymerases in amplification reactions \boldsymbol{\cdot}
                                                                                                                                                                                                   Examples; Fig 5; 18pp; German.
                                                                                                                                                                                                                                                                               WPI; 1999-602407/52.
                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE19818422-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat NF-1 DNA fragment 2.
                                                                                                                                                                                                                                                                                                                                          (HARJ/) HARJES
                                                                                                                                                                                                                                                                                                                                                                        24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              radiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NF-1; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ24099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ24099 standard; DNA; 240 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                    28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAACACCCAAGCCGGAGTCTCTCACAAGCTTGAATGTGTGTTCTGGAGCTGAAGGATGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATAGCTCCTGAGGAGGCCACAAAGGGAAATCTCCATTCATCTCTTCCTGCTACAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACGGCTGCTTAAGACGACTTAAGGGGGGAATGACGCAGCGGCTCTTAGAGGAACATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer; mutagenicity; mutation rate; polymerase error rate; \operatorname{\mathfrak{ss}}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                       98DE-1018422
                                                                                                                                                                                                                                                                                                                                                                                                     98DE-1018422
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PROSE SERVICE 
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AAA81467/
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Best Local Similarity
Matches 43; Conserv
08-OCT-1999;
                                                                                                      WO200022430-A2
                                                                                                                                                               Neisseria
                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification;
                                                                                                                                                                                                                                                                                                                    N. meningitidis partial DNA
                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                              AAA81467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .467/c
AAA81467 standard; DNA; 25509 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for monitoring nutrients or medicines and environmental factors such as radiation from televisions or computer screens. The method is applicable to all types of mutations (collectively or individually), is unaffected by repair mechanisms or in vivo selection mechanisms, and is an in vitro process so animal testing is not required. AA224098-Z24105 represent rat NF-1 DNA fragments used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method for determining the absolute mutagenicity of a substance. The method is used to determine the mutation rate associated with particular substances and the error rates for polymerases during amplification reactions. It is therefore useful for polymerases during amplification reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for determining absolute mutagenicity and polymerases in amplification reactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NF-1; rat; radiation;
                                                   20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 240 BP; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Examples; Fig 5; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-602407/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat NF-1 DNA fragment 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ24100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGGACAATCTGATGCTATATCTAAGAAAAACCTCCGTGCCAAGTCGAAGTTGCTTTT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTT 206
                                                                                                                                                          meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer; mutagenicity; mutation
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                             В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
99WO-US23573.
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                                                                                                                                                                                                             , diagnosis;
MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 53 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.88;
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Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                    sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 T; 0 other;
                                                                                                                                                                                                                                                                                                            gnm_15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rate; polymerase error rate;
                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                    H
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                                                                                                                                                                                                                                                                                                                    NO:15
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CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC represent specifically claimed Neisseria meningitidis genomic DNA
CC sequences; AAA81260 to AAA81303 and AAB2560 to AAB25663 represent
CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC SEQUENCES; AAA81304 to AAA81321 represent PCR primers used in the
CC AAA81452 represent Neisseria meningitidis DNA sequences; and AAA81322 to
CC AAA81452 represent Neisseria meningitidis DNA sequences; and AAA81322 to
CC CAAB1452 represent Neisseria meningitidis DNA sequences; and antibodies sequences, which are all used in the examplification of the present
CC composition can be used in the manufacture of a composition. The
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC exposed proteins all pathogenic Neissariae. Identification of sequences
CC medicament of vaccines against Meningococcus B; against all serotypes;
CC and/or against all pathogenic Neissariae. Identification of sequences
CC particularly organism-specific probes. Attempts to make efficacious
CC Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC Multivalent vaccines have also been tried but none have successfully
CC overcome antigenic variable. The provision of further, complete
CC sequences may provide an opportunity to identify secreted or surface
CC exposed proteins that may be presumed targets for the immune system and
CC other more variable regions
CC other more variable regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frazer CM, H
Masignani V,
        Sequence 25509 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other Neisserial infections, for example, N.gonorrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleotide sequences of Neisseria meningitidis used in the diagnosis and treatment of N. meningitidis \mathbf{i}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-1998;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Page 399-406; 1760pp; English.
                                                                            variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hickey E,
Galeotti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0103794
99US-0132068
6157 A; 6156 C; 6549 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peterson
C, Mora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥ (4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tettelin H, Venter
Ratti G, Scarselli
    6647
    H.
0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is which can a infection a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥, 'n
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and
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Query Match
Best Local Similarity
Matches 73; Conserv 8.8%; nilarity 52.5%; Conservative ; Score 33.4; D Pred. No. 8.4; O; Mismatches 8.4; DВ 66; 21; Length 25509; Indels 0 Gaps

0,

RESULT 11 AAF21607/ 23185 23305 TGATATAAAAATCATCCAAGAAAACATTAATAATTTTTGGAATAATTGTCCCTTTAATAT 23246 229 289 169 TGGAATAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGACTGT 228 CAGGTGGCGCAGCTATGTT 307 TGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAAT TAATTGGAGCAGCTATATT 23167

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X B X B X B X B X B

13-MAR-2001

(first entry)

Neisseria meningitidis B nucleotide sequence

SEQ ID

NO:108

AAF21607

standard;

DNA;

349980 BP

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                                                                                                   Query Match
Best Local
                                                                                            Matches
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Galeotti C,
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1999; 99US-0132068
08-OCT-1999; 99WO-US23573
28-FEB-2000; 2000GB-0004695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200066791-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-647603/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                        Claim 7; Appendix A; 692pp; English.
                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis B full length frames are used to detect, treat and
                                                                                                                                                                                                                                                                                                                                                                               Frazer CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                         Sequence 349980 BP; 84410 A; 84863 C; 94187
                                                                            169
                                                                                                   Local Similarity
         CAGGTGGCGCAGCTATGTT 307
                                                            TGGAATAAAAACCTCCCTGCCAAGTAGTACTTCGTTTTATGCTCAACATGCTTTGACTGT 228
                             TGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGATGGAGATGCCAATCCATGGAAT 288
TAATTGGAGCAGCTATATT 75730
                                                                                          73;
                                                                                                                                                                                                                                                                                                                                                                                               Hickey E,
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0132068.
99WO-US23573.
                                                                                                                                                                                                                                                                                                                                                                                       Peterson J, Tettelin H, Venter JC, Ratti G, Scarselli M, Scarlato V,
                                                                                                   52.5%;
                                                                                            ; Score 33.4; Di
; Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                        genome sequence and open reading prevent Neisserial infections -
                                                                                                            DB 21;
                                                                                                                            G; 86520 T; 0 other;
                                                                                              66;
                                                                                                            Length 349980;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                       Masignani V;
Rappuoli R;
                                                                                              0,
                                                                                              Gaps
                                                               75809
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ANX57669/c

ANX57669;

ANX ANX57669;
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14-SEP 2000
21-SEP 2000
21-SEP 2000
25-SEP 2000
25-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
20-OCT 2000
20-OCT
                        2000US-0234273
2000US-0234998
2000US-0234998
2000US-0235834
2000US-0235834
2000US-0235836
2000US-0236379
2000US-0236379
2000US-0236379
2000US-0237037
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2000US-0241785
2000US-0241785
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2000US-024178
2000US-024178
2000US-024178
2000US-024178
2000US-024178
2000US-024178
2000US-024171
2000US-024178
2000US-0241
RESULT 13
AAZ24101/c
ID AAZ241
XX
AC AAZ241
XX
DT 04-FEB
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynuclectides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent. (CC diagnose and treat immune/haematopoletic-related diseases, especially CC cancers and cancer metastases of haematopoletic antigen genomic CC sequences from the present invention. AAK5492 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
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P-PSDB;
                          04-FEB-2000
                                                                         AAZ24101;
                                                                                                                            AAZ24101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                             200
                                                                                                                                                                                                                                                                                                                                            177
                                                                                                                                                                                                                                                                                                                                                                                                                                      237
                                                                                                                                                                                                                                                                                                                                                                                          140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 TTAAGGGGGAATGACGCAGCGGCTCTTAGAGGAACATATGGAAAACACCCCAAGCCGGAGT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCTCTCACACATGATTTCATGTGCTCTGCCCCAATCCTGTAAAGTATTATAGCTCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTCACAAGCTTGAATGTGTGTTTTGGAAGCTGAAGGATGCACGGTTGTTAAGCCCCCTGT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-483426/52.
DB; AAM84888.
                                                                                                                                                                                                                                             GGTCTTT
                                                                                                                                                                                                                                                                                           TGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                     TCTTTTCCGTTGTTTAATCTAATGTTCTTTTGGAATAAAAACCTCCCTGCCAAGTAGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGGTGGGGAGGCTGCCCAAGTCAGAAATGGCAATTAAGAAAAACAAATGTACAGAACC
                                                                                                                                                                                                                                                                                                                                            TGTTTCTCAGGGGTTCGGTGAATGCTGCTTTTAAGGTTAACATGAATAGACAAWAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2729; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-025188.
2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0251990.
2000US-0254997.
2001US-0259678.
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                     (first entry)
                                                                                                                                                                                                                                                                                             206
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                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%;
48.1%;
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                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 2
Pred. No. 1.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM;
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T; 2 other; 22; 96;

Length 303 Indels

0;

Gaps

0

238

199

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RESULT 14
AAZ24102/C
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method for determining the absolute mutagenicity of a substance. The method is used to determine the mutation rate associated with particular substances and the error rates for polymerases during amplification reactions. It is therefore useful for monitoring nutrients or medicines and environmental factors such as radiation from televisions or computer screens. The method is applicable to all types of mutations (collective in individually), is unaffected by repair mechanisms or in vivo selection mechanisms, and is an in vitro process so animal testing is not required. AAZ24098-Z24105 represent rat NF-1 DNA fragments used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NF-1; rat; radiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE19818422-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-602407/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harjes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HARJ/) HARJES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-1998;
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                                                                                                                                                                                                                                                                AAZ24102 standard; DNA; 240
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examples; F1g 5; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerases in amplification reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for determining absolute mutagenicity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat NF-1 DNA fragment 4.
                                                                                                        DE19818422-A1
                                                                                                                             Rattus sp.
                                                                                                                                                       radiation;
                                                                                                                                                                 NF-1; rat;
                                                                                                                                                                                         Rat NF-1 DNA
                                                                                                                                                                                                                 04-FEB-2000
                                                                                                                                                                                                                                         AAZ24102;
                                                                                28-OCT-1999
          (HARJ/) HARJES
                                  24-APR-1998;
                                                        24-APR-1998;
                                                                                                                                                                                                                                                                                                                                          155 AATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTT 206
                                                                                                                                                                                                                                                                                                                             53 AATCTGATGCTATATCTAAGAAAAACCTCCGTGCCAAGTCGAAGTTGCTTTT 2
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 40; Conserv
                                                                                                                                                       primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer; mutagenicity; mutation rate; polymerase {\tt ss}.
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         B₽;
                                                                                                                                                                                        fragment 5.
                                                                                                                                                                                                                (first entry)
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                                  98DE-1018422
                                                          98DE-1018422
                                                                                                                                                                                                                                                                                                                                                                                                                       66 A; 52 C; 54 G; 68 T; 0 other;
                                                                                                                                                                  mutagenicity;
                                                                                                                                                                                                                                                                                                                                                                                     8.7%;
                                                                                                                                                                                                                                                                85
                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                          Score 32.8; D
Pred. No. 1.7;
0; Mismatches
                                                                                                                                                                  mutation rate;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                  polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       error rate
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                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                  240;
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                                                                                                                                                                  error
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RESULT 15
AAZ24103/C
ID AAZ24
XX
AC AAZ24
XX
AC AAZ24
XX
DT 04-F)
XX
DE Rat
XX
NF-1
KW NF-1
KW NF-1
XX
V NE-1
XX
V DE1
XX
V NE-1
V NE-1
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V NE-1
V NE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for determining the absolute mutagenicity of a substance. The method is used to determine the mutation rate associated with particular substances and the error rates for polymerases during amplification reactions. It is therefore useful for monitoring nutrients or medicines and environmental factors such as radiation from televisions or computer screens. The method is applicable to all types of mutations (collectively or individually), is unaffected by repair mechanisms or in vivo selection mechanisms, and is an in vitro process so animal testing is not required. AAZ24098-Z24105 represent rat NF-1 DNA fragments used to illustrate the method of the invention.
                       This invention describes a novel method for determining the absolute mutagenicity of a substance. The method is used to determine the mutation rate associated with particular substances and the error rates for polymerases during amplification reactions. It is therefore useful for monitoring nutrients or medicines and environmental factors such as radiation from televisions or computer screens. The method is applicable to all types of mutations (collectively or individually), is unaffected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 240 BP; 66 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Examples; Fig 5; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for determining absolute mutagenicity and error rate polymerases in amplification reactions \cdot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harjes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NF-1;\ rat;\ primer;\ mutagenicity;\ mutation\ rate;\ polymerase\ error\ rate;\ radiation;\ ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ24103;
                                                                                                                                                                                                                                                                                                                 Method for determining absolute mutagenicity polymerases in amplification reactions -
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-602407/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-1998;
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                                                                                                                                                                                                                                                            Examples;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harjes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARJ/) HARJES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
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nes 40; Conserv
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CC process so animal testing is not required. AAZ24098-224105 represent CC rat NF-1 DNA fragments used to illustrate the method of the invention. XX Sequence 240 BP; 66 A; 52 C; 54 G; 68 T; 0 other; Query Match 8.7%; Score 32.8; DB 20; Length 240; Best Local Similarity 76.9%; Pred. No. 1.7; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Matches 12; Indels 12;
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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## SUMMARIES

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AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX245292
Williams, L.T., Escopedo, J., Innis, M.A., Garcia, F.D., Sudduth Klinger, J., Reinhard, C., Randazzo, F., Rennedy, G.C., Pot, D., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M.,	Wammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 378)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.		AX245292.1 GI:15859966	AX245292	Sequence 222 from Patent WO0166753.	AX245292 378 bp DNA linear PAT 28-SEP-2001	

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Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M. Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATGACGCAGCGGCTCTTAGAGGGAACATATGGAAAACACCCCAAGCCGGGGCTCTCTCACA
TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT
                                           GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA
                                                                        GAATGACGCAGCAGCTCTGAGAGGAACATAAGGAAAACACCCCAAGCCGGAGTCTCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGCAGAAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGATGCCAATCCATGGAATCAGGTGGCACAGCTATGTTGGTAGCTATAGCAGAAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                         AX245365
Sequence
AX245365
                                                                                                                                                                                                                                                                                                        williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
                                                                                                                                                                                                                                                               Human genes and gene expression products Patent: WO 0166753-A 295 13-SEP-2001; Chiron Corporation (US); Hyseq Inc. (US)
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 322)
                                                                                                                                                                                                                                                                                                  Stache-Crain, B
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                            Conservative
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                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                                                                                                                                                                                                     295
                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
64 c 78 g 8
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 GI:15860039
                                                                                                                                                                                                                                                                                                                                                                                                                                    322 bp
from Patent W00166753
                                                                                                                                                                      74.0%;
98.6%;
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                                                                                                                                                            0;
                                                                                                                                                                    Score 279.6; DB 6
Pred. No. 1.4e-73;
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                                                                                                                                                            Mismatches
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with

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ACCESSION
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                                                                                                                                                                                       ACCESSION
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JOURNAL
                                                                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                         208 TGCTCAACATGCTTTGACTGTTGAAAAGAGACCCTTTGGCACACATTGAAGGGATGGTGAT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 GAATGACGCAGCAGCTCTGAGAGGAACATAAGGAAAACACCCAAGCCGGAGTCTCTCACA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 GAATGACGCAGCGGCTCTTAGAGGAACATATGGAAAACACCCAAGCCGGAGTCTCTCACA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGATGCCAATCCATGGAATCAGGTGGCACAGCTATGTTGGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGGATGGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genes and gene expression products Patent: WO 0166753-A 300 13-SEP-2001; Chiron Corporation (US); Hyseq Inc. (US) Location/Qualifiers
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1 (bases 1 to 318)

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D.,
Sudduth-Klinger, J., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.
Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M.,
Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 300 from Patent AX245370
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 59231)
                                                                                                                                                                                       AL135937
                                                                                                                                                                                                          Human DNA sequence from clone RP1 STSs and GSSs, complete sequence.
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  Phillimore, B
                                                                                            Homo sapiens
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/db_xref="taxon:9606"
63 c 76 g 8
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                                                                                                                                                                                                               59231 bp DNA linear rock to clone RP1-278022 on chromosome 20.
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                                                                                                                                                                                                                                                         PRI 15-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
IMPORTANT: This sequence is not the entire insert of clone RP1-278022 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP4-697P8 is at 59132 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality sendata (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP1-278022 is from the interest de jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on Mar 15, 2000 this sequence version replaced gi:7242336. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wit only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VECTOR: PCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the library RPCI-1 constructed by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //www.chori.org/bacpac/home.htm
                                                                                                                                                                                                             8546.
                                                               /note="13 copies 2 mer aa 96% conserved"
complement(10684. .11081)
                                                                                                                                                                                                                                                                                                                                          complement (5199
                                                                                                                                                                                                                                                                                                                                                 /note="MER58A repeat: matches 32.
complement(5199. .5709)
                                                                                                                                                                                                                                                                                                                                                                                                                                              3880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2927. .2992
/note="Alu repeat: matches 242.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                    note="match: GSS: Em:AQ662878"
                                                                                                                                 note="AluSq repeat: matches 1.
                                                                                                                                                                                    /note="
                                                                                                                                                                                                                                                                            /note="Charlie4a repeat: matches 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1ME2 repeat: matches 5541. .6154 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 3. .241 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MER3 repeat: matches 6. .191 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-
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'note="38 copies 2 mer aa 7.2% conserved'
                                                                                                                                                                                                                              'note="MIR repeat: matches 13. .81 of consensus"
                                                                                                                                                                                                                                                                                                                        note-"match: GSS: Em:AQ613263"
                                                                                                                                                                                                                                                                                                                                                                                                                   note-"LIM4 repeat: matches 4015.
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                                                                                                                                                                                  matches 7117. .7739 of consensus*
                                                                                                                                      .225 of consensus"
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/note**L2 repeat: matches 2195 .2293 of
13814 .14087
/note="AluY repeat: 31750. .32046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11575. .12292
/note="L1MA9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24124. .24510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (19364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 169.
complement(15295. .15803)
                                                                                             note="MER1B repeat: matches 1.
                                                                                                                   /note="L2 repeat: matches 2124.
30877. .31223
                                                                                                                                                                        /note="LlMC4 repeat: matches 7430. .7849 of consensus"
                                                                                                                                                                                                             /note="56 copies 2 mer ta 73%
                                                                                                                                                                                                                                          /note="LIMC4 repeat: matches 7841. .7973 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1M1 repeat: matches 5678. .5763 of consensus"
25134. .25443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="LTR16C repeat: matches 1. .387 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="34 copies 2 mer ga 79% conserved"
complement(19364. .19600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"match: GSS: Em:AQ694331"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L2 repeat: matches 2657.
                                                                                                                                                                                                                                                                                                                                            e="AluSq repeat: matches 1. .304 of consensus"
)5. .26579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :e="MIR repeat: matches 50. .139 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ce="MIR repeat: matches 26.
                                                                                                                                                                                                                                                                                                                                                                                                 e-"AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                                                       e="L1MC/D repeat: matches 5290. .5579 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e="match: GSS: Em:AQ035738"
2. .22242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .e="MIR repeat: matches 24. .50 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="MER58B repeat: matches 2. .341 of consensus"
1. .18717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e-"match: GSS: Em:AQ035618"
7. .13423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="LlME3A repeat: matches 5964. .6159 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e="L1ME3A repeat: matches 5427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9-"match: GSS: Em:AQ754141"
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                                                                                                                                                                                                                                                                                    "MIR repeat: matches 20. .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .24810
                                 "L2 repeat: matches 1945.
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                                                                                                                                                                                                                                 28583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            copies 2 mer ta 68% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 410. .521 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 17. .410 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 5545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1. .310 of consensus"
               matches 1. .309 of consensus"
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                                                                                                                                                                                                           conserved"
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                                                                                                                                   .2658 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                 .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .262 of consensus'
                                                  .2124 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .288 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2195 of
                                                                                             .337 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .6278
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                                      208
                                                                                                   148
                                                                GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA 18797
GTTGTTTAATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTA
                                                                                                                                     119;
                                                                                                                                   Conservative
                                                                                                                                                                                                 /note-"match: GSS: Em:AQ800109"
44765. .44818
/note-"MIR repeat: matches 200.
complement(45503. .46337)
                                                                                                                                                                                                                                                                 /note="LTR16C repeat: matches 165.
complement(43484..44004)
                                                                                                                                                                                                                                                                                                                                                                  /note="LIMA9 repeat: matches 3999. .4226 of consensus"
40380. .40675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="LIM3d repeat: matches 251. .280 of consensus"
39314. .39717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32189. .32474
/note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSg repeat: matches 3. 32047. .32188
                                                                                                                                                                                                                                                                                                               note="L1MA9 repeat: matches 4226.
                                                                                                                                                                                                                                                                                                                                             /note="AluJo repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                  39992. 40126
/note="AlluJo repeat: matches 2. .134 of consensus"
40153. .40379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L2 repeat: matches 1420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L2 repeat: matches 1809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="MSTB repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8841. .39254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="MIR repeat: matches 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 84. .150 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7904. .37941
note="19 copies 2
                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"LlMA9 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="LlM3e repeat: matches -879. .779 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21. .36273
e="MIR repeat: matches 66.
                                                                                                                                31.5%; Score 119; DB 9;
100.0%; Pred. No. 5.3e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .39304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mer aa 81%
                                                                                                                                                                                                                                                                                                                                                                                                                                             matches 3735. .4011 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .426 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .84 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .225 of consensus"
                                                                                                                                                                Length 59231;
                                                                                                                                                                                                                  . 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .261 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1937 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .298 of consensus"
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                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                  . 386
                                                                                                                                                                                                                                                                                                                  .6308
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                                                                                                                                                                                                                  consensus"
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ACCESSION VERSION KEYWORDS RESULT 6 AC119775/c SOURCE DEFINITION LOCUS ORGANISM

REFERENCE AUTHORS Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; (
Mammalia; Eutheria; ! AC119775 AC119775.4 GI:21747184 HTG; HTGS\_PHASE1. AC119775 162394 bp DNA Rattus norvegicus clone CH230-464J18, \*\*\*\*, 61 unordered pieces. Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Rattus. (bases 1 to 162394) Chordata; Rodentia; Craniata; Vertebrata; Sciurognathi; Muridae; SEQUENCING ·linear Euteleostom1;
; Murinae; HTG 18-JUL-2002 IN PROGRESS

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

as soon as i be preserved

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Delaney, K. R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J.,
Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M.,
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Li, J., Li, Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Lozado, R. J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J.,
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2 (bases 1 to 162394)
Worley,K.C.
Direct Submission
Submitted (02-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 162394)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Caveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Davis, C., Davy-Carroll, C., Davy-Carroll, C., Davy-Carroll, L., Davis, C., Davy-Carroll, C., Davy-Carroll, L., Davis, C., Davy-Carroll, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:20467838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
Direct Submission
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 104933 bases at least Q40
Consensus quality: 117540 bases at least Q30
Consensus quality: 117408 bases at least Q30
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45206: contig
45306: gap of
47814: contig
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51910: contig
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Mouse DNA
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 28, 2002 this sequence version replaced gi:21531387.
                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 223604)
                                   Submitted (27-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                        Dunn, M.
                                                                                           Mus musculus
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                                                                                         Submitted (04-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: zface@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 176543)
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                                                        Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL845312.1 GI:22205007
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Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Wellcome Trust Sanger Institute Center code: SC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20135 TGGACGTGTTCAACATGCAATAAATGTGGATAAGACCAATGAAGCACTTTTTGAAGGC 20076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 ATGGTGATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 TGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGG 259
                                                                                                                                                                                                                                                                                                                                                                        320 AGAAGTCTTCTTGGCAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTTTCAGTATAAAACAATTAGTCGCATCACAAGGCTCTCCAAAGTTTCATGCAATTTC 20016
                                                                                                                                                                                                                                                                                                                             GGGTGTTTCATTTTAA 19999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry: Dye-terminator; 100% of reads Consensus quality: 175506 bases at least Q40 Consensus quality: 175596 bases at least Q30 Consensus quality: 176033 bases at least Q20 Consensus quality: 176033 bases at least Q20 Insert size: 176343; sum-of-contigs Insert size: 176343; sum-of-contigs Insert size: 176343; sum-of-contigs Quality Quality Coverage: 10.13x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: zK287F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coverage: 10.57x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: zface@sanger.ac.uk
                                                                                                                                       Rattus norvegicus clone CH230-9H1,
67 unordered pleces.
AC129650
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                 HTG; HTGS_PHASE1.
Norway rat.
                                                                                                                                                                                                             AC129650
                                                                                                                 AC129650.1 GI:22024419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57205
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/note="assembly_fragment:02085

fragment_chain:1"

166620 .176543
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1. .176543
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31955 c 31568 g 55615 t 20
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Danio rerio"
/db_xref="taxon:7955"
/clone="DKEY-287F10"
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165519: contig of 96228 bp in length
165519: config of 96228 bp in length
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*** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
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TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

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Bouck, J., Bowle, S., Birleva, M., Brown, R., Brown, N., Brydt, N., Bowle, S., Burch, P., Burkett, C., Burchl, K., Byrd, N.C., Chard, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cheveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K. R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K. R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K. R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K. R., David, R., Carroll, L., Dederich, D.A., Delaney, K., R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K., R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K., Barlis, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Escotto, M., Escotto, M., Carroll, J., Garza, M., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, M., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, M., Gill, R., Garlis, T., Gabisi, A., Garcia, A., Garner, T., Garza, M., Gill, R., Gao, J., Garcia, A., Garner, T., Garza, M., Gill, R., Gao, J., Garcia, A., Garner, T., Garza, M., Gill, R., Gao, J., Garcia, A., Garner, T., Garza, M., Gill, R., Gao, J., Garcia, A., Hogues, M., Hollows, C., Hentico, K., Hernandez, J., Harris, K., Harris, K., Harris, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, M., Garza, M., Gill, R., Jackson, L., Halle, S., Joudh, S., Jackson, L., Haber, J., Hulyk, S., Hume, J., Jackson, L., E., Homsi, F., Homsi, F., Homsi, S., Joudh, S., Joudh, S., Kratovic, J., King, L., Korah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lil, J., Lil, M., Loulseyed, H., Lozado, R., Martinez, E., Mahsen, J., Lucler, R., Martindale, A., Martinez, E., Mahsen, J., Lucler, R., Martindale, A., Martinez, E., Marten, S., Patch, M., Ren, Y., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C.
Direct Submission
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Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 115101 bases at least Q40
Consensus quality: 120951 bases at least Q30
Consensus quality: 125022 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: GDLF
Center clone name: CH230-9H1
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This record will as soon as it is be preserved.
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Arabidopsis thaliana chromosome complete sequence.
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Spriggs, T.A., Mason, T.M., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-FEB-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.or On Apr 18, 2002 this sequence version replaced gi:6598350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medical Center Dr., R
3 (bases 1 to 91071)
Town, C.D. and Kaul, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Direct Submission
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KPVWQAVENQCRVFATCGSQVCSFNSSGYTECKCPFNAFVSVSUDKCLVPPQKPGKSK
GFNWAVFKNLELYGIYPANDSVISQISSQRCKKLCLENSACTAVTYTNDGEPQCRWKL
TRYISGYSDPSLSSISYVKTCLDPIAVDPNNVSKESPVTVTKSHSICIPCLVGATSTT
LVLFLGFQLGIVYYIYRRKKKLAKKKAERFSKATNPKGVMIFSVDEIKAMTDNTDNNI
LVLFLGFQLGIVYYIYRRKKKLAKKKAERFSKATNPKGVMIFSVDEIKAMTDNTDNNI
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ELVLFDSLLGVPVWNSKTNRFSVSSALLRDDGNLVLLKDREEIVWQSFGTPTDTLLPN
QKFPAFEMLRAASENSRSSYXSLHLEDSGRLELRWESNITFWSSGNEVVKKKKKKKNI
                                                                                                                                                                                                                       complement(join(<3329. .3541,3637. .3727,3807. .3852,
3927. .4062,4153. .4274,4362. .4724,4801. .4930,5029.
5183. .5296,5446. .5500,5725. .5857))
/gene="At2g41880"</pre>
                                                                                                                                                                                                                                                                                                                                                                                complement(3329. .5857)
/gene="At2g41880"
                                                                                                                         complement(join(3460...3541,3637...3727,3807.3927...4062,4153...4274,4362...4724,4801...495183...5296,5446...5448))
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184. .2478
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/chromosome="2"
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/cultivar="Columbia"
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/protein_id="AAM14823.1"
/db_xref="G1:20196890"
/translation="MKMLRALLLCLSLVFFLAFQIVVSEIQLGSKLVVGENTLWVSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene-"At2g41890"
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                     /product="putative guanylate kinase"
/protein_id="AAM14825.1"
/db_xref="GI:20196895"
                                                                                                                                                                                                                                                                                                                                                note="T11A7.23; supported by cDNA: g1_7861794_gb_AF204675
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translation-"MGEAPAVLVDHPENGHSNGVCVKSEPENTEITVDVGDRIFLIGG/
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FPSNMFGFSVSHTTRSPRSMENDGVHYHFADKKVMEKEINGGKFLEFASVHGNLYGTSI
ESVERAVTDSGKRCILDIDUOGARSVERASSLDAIFIFVCPPSMKELEDBLRARGTETEE
QIQKRLRNAEAEIKEGISSGIFGLILYNDNLEECYKKLKNLLGLDGLAHVNGVEIEGI
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/rpt_family="(GAA)n"
join(8017...8640,9217...9417)
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                                                                                                                                                                                                                                                                                                                                                                                                                       complement(15877. .15 /rpt_family="AT_rich" 16477. .18618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Traislation="MGNCCGTAGSLIQDKQKKGFKLPNPFSNEYGNHHDGLKLIVLKE
PTGHEIKQKYKLGRELGRGEFGVTYLCTEIETGEIFACKSLIKKKTSIDIEDVKRE
PTGHEIKQKYKLGRELGRGEFGVTYLCTEIETGEIFACKSLIKKKTSIDIEDVKRE
VEIMROMPEHPNIVTLKETYEDDKAVHLYMELCEGIELDFAIVARGHYTERAAASVIK
TIIEVVOMCHKHGVMARDLKPENFLFANKKETASLKALDFGLSVFFKPGTERAAASVIK
TIIEVVOMCHKHGVMARDLKPENFLFANKKETASLKALDFGLSVFFKPGTERAAASVIK
PTYMAPEVLRSYGQEIDIWSAGVILYILLCGVPPFWAETEHGVAKAILKSVIDFKRD
PMFKYSDNAKOLIKKMLHPDFBRRTLTAQOVLDHPWIONGKNASUVSLGETVRARLKQF
SYMNKLKKRALRVIABHLSVEETSCIKERFGVMDTSNKGKITITELGIGLQKLGIVV
PODDIOILMDAGDVDKOGYLDVNEFVAISVHIRKLGNDEHLKKAFTFFFDKKKGYIEIE
ELRDALADDVDTTSEEVVEAIILDVDTNKDGKISYDEFATMMKTGTDWRKASRQYSRD
LFKCLSLKLMQDGSLQSNGDTK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(10329...10
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEKTQNNVAKAQRKAEERRATAEAKRGTEVAKVVEVANLMRALGRPPAKRSFFSFS*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mltlyhqerspdatsndrdetpetvvrevhaltpapednsrtmt
atlppppafrgyfspprsattmsegenfttisrefnalviagssmennelmtrdvtqr
ederqdelmrihedtdheeetnplaivpdqypgsgldpgsdnapgqsrygstvqrvkr
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/protein_id="AAM14826.1"
/db_xref="GI:20196896"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLPIEYAVSKMEDKIIIQETGKETRNKIVVDISSLNGGAPGRTRGILVDAIKF*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AT_rich" complement(14694...14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8642. .8664)
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/gene="At2g41870"
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/note="T11A7.3; supported by cDNA: g1_11908071_gb_AF326883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative calcium-dependent protein kinase"
/protein_id="AAM14824.1"
/db_xref="GI:20196892"
                                                                                                                                                                                                                                                      join(<16477. .16731,16830. .16961,17046. .17216,17458. .17665,
17823. .17904,17999. .18107,18206. .18319,18409. .>18618)
/gene="At2941850"
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17823. .17904,17999. .18107,18206. .18319,18409. .18618)
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                                                                                  /product="putative polygalacturonase"
/protein_id="AACO2763.1"
                                                                                                                                                                                                                                                                                                                                                        /gene="At2g41850"
/note="T11A7.5"
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.12327,12415 .12645,12735 .12890)
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2327,12415. .12645,12735. .>12890)
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ACCESSION
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                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                              CTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAACATGCTTTGAC 225
                                                                                                                                                                                                                                            AGTTAAACGTAAAGCTTAATTAAACAAAGAACAAAT 41639
                                                                                                                                                                                                                                                                                    TGTTGAAAAGAGACCTTTGGCACACATTGAAGGGAT 261
                                                                              Homo sapiens BAC
AC104652 AC034273
AC104652.3 GI:18
                Homo sapiens
                                                                                                                                            AC104652
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1011(24083. .24229.2/407
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complement(17300. 17333)
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DGGDTGVVDGNGETW#QNSCKRNKARALTFYNSKSLIYKNLKYRNAQQIQISIEKCSN
VQVSNYVTAPADSPNTDGIHITNTQNIRVSSIIGTGDDCISIESGSQNVQINDITC
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MDNVKNPIIIDQDYCDKSKCTTEKSAVQVKNVYYRDISGTSASENAITFNCSKNYPCQ
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IMPVQKQTRAGQRTREKAFVVVGDGNGHVGLGVKCSKEVATAIRGAIILAKLSVVPVR
RGYMGNKIGKPHTVPCKVTGKCGSVTVRMVPAPRGSGIVAARVPKKVLQFAGIDDVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(24083...24229,24605...24679,24862...24986,25189...25303,
25475...25558,25660...25707,25758...25871,26076...26241,
26613...26905,27234...27749,27973...28122,28266...28341,
28553...28680,28855...29049,29166...29303,29391...29501,
29500...29839,29941...30105)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="At2g41830"
/note="T11A7.7; predicted by genscan; similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="40S ribosomal protein S2"
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join(19138. 19833,20359.
/gene="At2g41840"
/codon_start=1
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/note="T11A7.6; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MAERGGERGVERGGERGDFGRGFGGRGGRGDRGGRGGRGGRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="At2g41830"
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Metazoa;
                                                                                GI:18464293
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5. .18742
                                                                                                                     130206 bp
clone RP11-273F23
Chordata; Craniata;
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Vertebrata;
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                                                                                                                                                                                                                                                                                                              Submitted (21-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Feb 1, 2002 this sequence version replaced gi:18087701.
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Submitted (01-FEB-2002) Genome
University School of Medicine,
MO 63108, USA
5 (bases 1 to 130206)
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Direct Submission
Submitted (18-DEC-2001) Genome Sequencing Center, Washington Center, Wash
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3 (bases 1
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The sequence of Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                         Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Drafting Center: WIBR
                                     Center project name: H_NH0273F23
                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
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s BAC clone RP11-273F23
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                                                                                                                                                                                                                                                                                                                                                                                                       63108, USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc INFORMATION: Louis

## SOURCE INFORMATION:

밁 Š 밁 δ 문 ş

The RPCI-11 human BAC library was made from the blood of one donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenç Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.chori.org pBACe3.6 f one male Frengen, E., from

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-679C8, 2000 bp overlap.
Actual start of this clone is at base position 1 of RP11-273F23;
actual end is at base position 61045 of RP11-679C8.

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FEATURES
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         /rpt_family="ERV1"
24408. .25160
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/db_xref="taxon:9606"
                                                              /rpt_fam1ly="(TAGA)n"
23577. .23811
                                                                                                                                                                       /rpt_family="L1"
22477. .22755
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rpt_family="ERV1"
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7. .17679
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9. .23213
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Homo sapiens BAC clone RP11-44D21 from
AC108866
AC108866.5 GI:19848440
                                                                                                                                                                                                                                                                                                            66;
 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 153822) Sulston, J.E. and Waterston, R.
                                                                     Homo sapiens.
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llarity 58.9%;
Conservative
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25580. .26611
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6. .30767
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7. .30735
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5. .29100
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Genome Res. 8 (11), 1097-1108 (1998)
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9847074
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Submitted (30-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (21-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (31-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-ARR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Mar 30, 2002 this sequence version replaced g1:19570183.
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  NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-44D21;
actual end is at base position 152822 of RP11-44D21.
                                                                                                         The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                         SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                sequence, see http://genome.wustl.edu/gsc
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                                                                                        VECTOR:
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/rpt_family="CR1"
31674. .32256
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29527. .2
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26710..2
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24563
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20537. .20557
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9364. .9454
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/chromosome="4"
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SOURCE
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Homo sapiens chromosome 10 clone RP11-435B15 map 10,
SEQUENCE, 18 unordered pieces.
ACO80170
1 (bases 1 to 190912)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 10, clone RP11-435B15
                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                               AC080170.2 GI:12830207
HTG; HTGS_PHASE1; HTGS_DRAFT.
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45308. .45339
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45261. .45307
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Pred. No. 1
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.960731 Consensus quality: 184508 bases at least 040 Consensus quality: 187307 bases at least 030 Consensus quality: 189400 bases at least 020

Center project name: L10588
Center clone name: 435\_B\_15
------ Summary Statistics
sequencing vector: Plasmid; n/a; 100% of reads

Contact: sequence\_submissions@genome.wi.mit.edu

Web site: http://www-seg.wi.mit.edu

Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR

Research

Insert size: 198000; agarose-fp
Insert size: 189212; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 5.1 in Q20 bases; sum-of-contigs

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CE 2 (bases 1 to 190912)

BB BITEON B. Linton, L. Nusbaum, C., Lander, E., Abraham, H., Allen, N., Baderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dakrellano, K., Dewar, K., Dhaz, J.S., Dodge, S., Perteira, P., Lamazares, R., Landers, T., Lebockky, J., Levine, R., Lieu, C., Liu, G., Kandonald, P., Marquis, N., McCarthy, M., McDan, P., McKernan, K., McDarthy, M., McDan, P., McKernan, K., McDan, P., McKernan, K., McMan, P., McKernan, K., McMan, P., McKernan, M., McDan, P., McKernan, M., McDan, P., McKernan, M., McDan, P., McKernan, K., McDan,
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8805 8904: gap of 100 bp
8905 9991: contig of 1087 bp in length
9992 10091: gap of 100 bp
10092 11974: contig of 1883 bp in length
11975 12074: gap of 100 bp
12075 14089: contig of 2015 bp in length
14090 14189: gap of 100 bp
14190 15997: contig of 1508 bp in length
1598 18961: contig of 3064 bp in length
18862 18961: gap of 100 bp
18863 18961: gap of 100 bp
18863 18961: gap of 100 bp
18863 18961: gap of 100 bp
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136744 136843:
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                               /note="assembly_fragment"
28884. .33590
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/db_xref="taxon:9606"
/chromosome="10"
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/clone_lib="RPCI-11 Human
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10092. .11974
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3227: gap of 100 bp in length
136743: contig of 46516 bp in length
36843: gap of 100 bp in length
173143: contig of 36300 bp in length
73243: gap of 100 bp
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90127: contig of 13210 bp in length
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3839: contig of 2068 bp in
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                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
           Direct Submission
Submitted (28-JUN-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                              Direct Submission
Submitted (28-MAR-2000)
University, 4444 Forest
5 (bases 1 to 30960)
                                                                                                                                                                                            Submitted (01-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                      The sequence of C. elegans cosmid Y46C8AL Unpublished (2001)
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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42375. .51118
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173244. .190912
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Pred. No. 1.
                                                                                                 Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFecome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from Blastx analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program trNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Aventouis, MO 63110, USA Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysis see:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cosmid is F56D6, 200 bp overlap; the 3'
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/product="Hypothetical protein Y46C8AL.3"
/protein id="AAF60598.1"
/db_xref="GI:7331910"
/tanslation="MLIKFIFELSTLAGLASAVCPDSNDHEVQGFCFKFVAQQMTYTD
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DNGSPVGYTNLGSQNGNNLYFTESLANTKWNTLGDDKINYFVCSYNPATTPTTPSTTT
                                                                                                                                                                                                                                                                                                                                                             /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seg/sequence?name=Y46C8AL.3;cla
ss=Sequence"
                                                                                                                                                                                                                             'gene-"Y46C8AL.3"
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3004. .3097,4144. .4383,4441. .4585,4636. .4733,4784. .4905
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/protein_id="AAP60602.1"
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/db_xref="GI:
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AFYARSAFGGSAESFWIGLSRWGSGSLSWIDNGFVYITNFGSKYGNNYFTEKISNSK
WYTPGDNETHYLEVCSYDPTVQPVTGKATTPGTTTTAANVNCOFGARGTVLFAYSNDFE
PYIVQNTFSNSILYKQQVTFAIIRFDTRQPGSIMYFNDYNQALAYVRNHLPDYKLGFQ
ESTTGSDVLDVINNFYNNSSACASVVMVLSRRYPNTPDISRTVAKVRQYHGINVFLAS
NVPFGGSQSQVLFDLASQTNGLYGIEQDSLFSKRILYMPLRTRYPIYAVNAKVSGEGF
QVLPPMSVPQFDDFLIMYSVGSHLPVSNVQYVNLKWYMPSFPYSDKFEMQDYVMDSNT
NYNTITIGLSQNYYNMTIDYITNTDVETMQIRLXSSYFTNYMLPYSN*
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GFGDTKTGSNVLDVIDKFYDNTKLTPCGSIVMVLLKRYSNSNDISNIVAKVRKHHGSV
NFIASNTPSGGTNSRVLFDLSSRTNGLYVIDRDSYFMQSIDMMFLIERYPIYAANPVV
MTIDYIYTNTDVETMQIRFYSSL"
                                                   YNDISSCGSVVMVLSKRYPNTMDISSTVAKVRQYHGMVNFLASNAPSGGTQSRVLFDL
SSRINGIYSIEEDAIFLHFIGWMPLRERYPIYAVNVKVSGHGSQVLPPMSVPRDVTYL
IMVSLQSHLPISNVQSAKLNWFNPPFPQGALSWQPSEWAYTNSNSGGNRRIIDPAVYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=Y46C8AL.5;cla
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NELFVCYHENMCIISQVLSECKLKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(8898. .9932,10290. .10334))
/gene="Y46C8AL.2"
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/note="fer
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http://www.wormbase.org/db/seq/sequence?name=Y46C8AL.4;cla
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WNNPYTNANGKRANLDASGFAMTVEYVYNDSGDHPMQIRFYSPEATDFWLPYTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(12224. .12333,12381. .12503,12615. .12780,1:
13870. .14145,14204. .14387,14441. .14534,15204.
15486. .15630,15678. .15772,15826. .15951)
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/translation-"MTYDDAHNWCHFKNPVGNKANAKYNEVYTDYSDYHQVYSDYSDY
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/protein_id="AAF60597.1"
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7159,7390. .7623,8127. .8271,8322. .8416,8469.
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/note="for a graphical representation of this gene see: http://www.wormbase.org/db/seq/sequence?name=Y46C8AL.6;cla

16234. .21008 /gene="Y46C8AL.6"

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REFERENCE
AUTHORS
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AL732628/c
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1668 GAACATATGCCAGATAGGAAGAGCCTACTGG 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 AATCTAATGTTCTTTGGAATAAAAACCTCCCTGCCAAGTAGTACTTGGTTTTATGCTCAA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 CATGCTTTGACTGTTGAAAAGAGACCTTTGG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL732628 174196 bp
Danio rerio clone CH211-144F18,
                                                                                                                                Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 173595 bases at least Q40
Consensus quality: 173741 bases at least Q30
Consensus quality: 173741 bases at least Q20
Insert size: 173996; sum-of-contigs
Insert size: 161892; 19.9% error; agarose-fp
Quality coverage: 6.72x in Q20 bases; sum-of-contigs Quality
coverage: 7.22x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: zface@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug.11, 2002 this sequence version replaced g1:21911655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidomes; Cyprinidae; Danio.

1 (bases 1 to 174196)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: zC144F18
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
Contact: zface@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corby, N
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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/db_xref="G1:7331915"
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/translation="MRASRRPHAGRERADARRCVWEMKCERLFURDARGLPVYYNEFGKNIG
IXYFDSVTSNNLASHARIAFGPAAKNEWIGLSKNIGSSCLSWDDGLPVYYNEFGKNIG
IXYFDSVTSNNLASHARIAFGPAAKNEWIGLSKNIGSTSPEFLRORSVPWHISCHDFVE
IXYFDSVSNAKWNILGDNDTWFYCSSDSAGNESTFPEFLRORSVPWHISCHDFVE
ILPQHFGYIEHRRESSKIFRNNQLTOBDRIFDCALDRLISLKLNKULISWIIAFLIN
RVFQYKVGDSLSSFKKADCGVPQGAVLSPLLFGIFVNEIPNILPPAIKCKQFADDLKL
YTAIPSNSNNNVHLQKAIETIYEWSKATKLALNNDKTYCISLGRUTTEEGYTIENSLI
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join(16234.
19338. 19628
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/gene="Y46C8AL.6"
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. .19628,20472. .20616,20666. .20763,20809. .20930,
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Pred. No. 1.5;
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WOGRESS ***, 3
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Search completed: January 31, 2003, 03:21:40 Job time : 3850 secs

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ORIGIN
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Best Local Similarity
Matches 75; Conserv
                                                                                                                                             98366 TGGACGTGTGTTCAACATGCAATAAATGTGGATAAGACCAAGGAAGCACTTTTTGAAGGC 98307
                                                                        98306
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                                                                                                                                                                                   200 TGGTTTTATGCTCAACATGCTTTGACTGTTGAAAAGAGACCTTTGGCACACATTGAAGGG 259
GGGTGTTTTATTTTTAA 98230
                                   AGAAGTCTTCTTGGCAA 336
                                                                      AAGTTCCAGTATAAAACAATTAGTCGCATCCCCAGGCTCTCCAAAGTTTCATGCAATTTC 98247
                                                                                                          ATGGTGATGGAGATGCCAATCCATGGAATCAGGTGGCGCAGCTATGTTGGTAGCTATAGC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number wil
be preserved.
                                                                                                                                                                                                                                                                                                                 59260 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53762 53861: gap of 100 bp
53862 77324: contig of 23463 bp in length
77325 77424: gap of 100 bp
77425 174196: contig of 96772 bp in length
Location/Qualifiers
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:01503
fragment_chain:1"
77425. .174196
                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment:00262
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                               53862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Danio rerio"
/db_xref-"taxon:7955"
/clone-"CH211-144F18"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment:00869
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_11b-"CHORI-211"
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Pred. No. 2;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                                                                                   200 others
                                                                                                                                                                                                                                                            Length 174196;
                                                                                                                                                                                                                        Indels
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